

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 19:51:27 ; Search time 60 Seconds  
(without alignments)  
1099.318 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPNTVLPYQTP.....KLNLFNIADAFGVGKSSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

- 1: /SID32/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SID32/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SID32/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SID32/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SID32/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SID32/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SID32/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SID32/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SID32/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SID32/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SID32/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SID32/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SID32/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SID32/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 15: /SID32/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 16: /SID32/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 17: /SID32/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 18: /SID32/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 19: /SID32/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SID32/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SID32/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SID32/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	23	Arabidopsis CDPK2
2	2458	94.8	501	21	Arabidopsis thalia
3	2458	94.8	501	23	Arabidopsis CDPK4
4	2064	79.6	425	21	Arabidopsis thalia
5	1932	74.5	512	20	Soybean CDPK prote
6	1924	74.2	399	21	Arabidopsis thalia
7	1742	67.2	483	21	Arabidopsis thalia
8	1742	67.2	556	21	Arabidopsis thalia
9	1703	65.7	856	21	Arabidopsis thalia
10	1703	65.7	893	21	Arabidopsis thalia

11	1703	65.7	1017	21	AAG38597	Arabidopsis thalia
12	1509.5	59.2	549	23	AAG52842	Physcomitrella pat
13	1509	58.2	408	21	AAG31159	Arabidopsis thalia
14	1501	57.9	463	21	AAG46565	Arabidopsis thalia
15	1500	57.8	280	22	ATCDPK2 kinase dom	Arabidopsis thalia
16	1462	56.4	529	21	AAG29590	Arabidopsis thalia
17	1462	56.4	542	21	AAG29589	Arabidopsis thalia
18	1460.5	56.3	459	21	AAG29591	Arabidopsis thalia
19	1457	56.2	569	15	AAR56237	Protein kinase spe
20	1325.5	51.1	538	21	AAG43621	Arabidopsis thalia
21	1319	50.9	404	21	AAG46566	Arabidopsis thalia
22	1187.5	45.8	307	20	AAG46567	Tobacco CDPK prote
23	1166.5	45.0	424	21	AAG43622	Arabidopsis thalia
24	1166.5	44.5	421	21	AAG43623	Arabidopsis thalia
25	1153.5	44.5	421	21	AAG43623	Arabidopsis thalia
26	1059	40.8	413	22	AAG65755	ATCDPK kinase doma
27	1015.5	39.2	523	21	AAG10101	Arabidopsis thalia
28	928.5	35.8	426	21	AAG10102	Arabidopsis thalia
29	920.5	35.5	302	21	AAG54428	Zea mays protein f
30	900	34.7	274	22	AAG65756	ATCDPK1 kinase dom
31	887	34.2	274	19	AAW49837	Amino acid sequenc
32	887	34.2	274	22	AAG65757	ATCDPK1A Kinase do
33	887	34.2	274	22	AAG65759	ATCDPK1A PK domain
34	849	32.7	597	23	AAW52841	Physcomitrella pat
35	842.5	32.5	384	21	AAG10103	Arabidopsis thalia
36	829	32.0	623	22	AAB85583	Rice CDPK (clone r
37	771.5	29.8	456	16	AAR74996	E. maxima Em70-1 a
38	753.5	29.1	504	21	AAG16593	Arabidopsis thalia
39	753.5	29.1	594	21	AAG16592	Arabidopsis thalia
40	737	28.4	502	21	AAG53884	Arabidopsis thalia
41	737	28.4	594	21	AAG53883	Arabidopsis thalia
42	712.5	27.5	428	21	AAG16594	Arabidopsis thalia
43	712.5	27.5	524	21	AAB18394	Plasmodium falcipa
44	694.5	26.8	189	23	ABG59978	Human DITP polype
45	690.5	26.6	414	21	AAG53885	Arabidopsis thalia

ALIGNMENTS

RESULT 1  
AAM48000  
ID AAM48000 standard; Protein; 495 AA.

XX AAM48000;

XX 08-MAR-2002 (first entry)

XX Arabidopsis CDPK2 SEQ ID NO 1.

DE Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;  
KW disease resistance; agricultural; pathogen; crop yield; ornamental;  
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;  
KW transgenic; plant; enzyme.

OS Arabidopsis thaliana.

XX WO200184911-A1.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US14368.

XX 05-MAY-2000; 2000US-201925P.

XX (GEO ) GEN HOSPITAL CORP.

XX Sheen J;

XX WPI; 2002-062179/08.

XX N-PSDB; ABA06021.

XX Producing plant having increased disease resistance, comprises

PT

PT regenerating plant from a non-naturally occurring plant cell  
PT over-expressing a polynucleotide encoding a calcium dependent protein  
PT kinase polypeptide  
XX  
XX  
XX Disclosure; Fig 1; 44pp; English.  
XX  
CC The invention relates to producing a plant having increased disease  
CC resistance, comprising providing a non-naturally occurring plant cell  
CC over-expressing a polynucleotide encoding a calcium dependent protein  
CC kinase (CDPK) polypeptide and regenerating a plant from the plant  
CC cell, where the CDPK polypeptide is expressed in the plant, increasing  
CC the resistance of the plant to disease as compared to a  
CC naturally-occurring plant. The method is useful for a variety of  
CC agricultural and commercial purposes including improving a plant's  
CC resistance against plant pathogens, increasing crop yields, improving  
CC crop and ornamental quality and reducing agricultural production costs.  
CC The method facilitates an effective and economical method for in-plant  
CC protection against plant pathogen, reducing or minimising the need for  
CC traditional chemical practices (e.g. application of fungicides,  
CC bactericides, nematocides, insecticides, or vorticides) that are typically  
CC used by farmers for controlling the spread of plant pathogens and  
CC providing protection against disease causing pathogens. The method  
CC contributes to the production of high quality and high yield agricultural  
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
CC having reduced spots, blemishes and blotches that are caused by  
CC pathogens, agricultural products with increased shelf-life and reduced  
CC handling costs and high quality and yield crops for agricultural  
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis  
CC thaliana CDPK2 of the invention.

XX	Sequence	495 AA;
XX	Query Match	100.0%; Score 2593; DB 23; Length 495;
XX	Best Local Similarity	100.0%; Pred. No. 2e-222;
XX	Matches	495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	METKPNRPNTVLPYOTPLRDHYLLGKLGQGGTGYLTCTEKSANYACKSIPKR 60
DB	1	METKPNRPNTVLPYOTPLRDHYLLGKLGQGGTGYLTCTEKSANYACKSIPKR 60
QY	61	KLVCREDYEDVWREIQIMHLSHEPNVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120
DB	61	KLVCREDYEDVWREIQIMHLSHEPNVRIKGTVEDSVFVHVMVECGGELFDRIVSKG 120
QY	121	HFSEAEVKLIKTILGVVEACHSLGWHRDLKPNFLPDSKDDAKLKATDFGLSVFYKP 180
DB	121	HFSEAEVKLIKTILGVVEACHSLGWHRDLKPNFLPDSKDDAKLKATDFGLSVFYKP 180
QY	181	GOYLVDVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB	181	GOYLVDVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY	241	GKLDKSDPWPITSEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKPLDPAVL 300
DB	241	GKLDKSDPWPITSEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKPLDPAVL 300
QY	301	SRLKQSQNNKIKKMLRVIAERLSEEEIGGKELFKMTDNTNSGTTIFEEKAGLKVKG 360
DB	301	SRLKQSQNNKIKKMLRVIAERLSEEEIGGKELFKMTDNTNSGTTIFEEKAGLKVKG 360
QY	361	SELWSEIKSLMDAADIDNSGTTIDYGEFLAATLHMKNQWEREILVAAFSDFDKDGSGYIT 420
DB	361	SELWSEIKSLMDAADIDNSGTTIDYGEFLAATLHMKNQWEREILVAAFSDFDKDGSGYIT 420
QY	421	IDELQSACTEFGLCDTFLDMDIKEDLDNDGKIDFSEFTANMKGGGVGRSRTMMKNLNF 480
DB	421	IDELQSACTEFGLCDTFLDMDIKEDLDNDGKIDFSEFTANMKGGGVGRSRTMMKNLNF 480
QY	481	NIADAFGVDCGKSD 495
DB	481	NIADAFGVDCGKSD 495

RESULT 2	
AAG35776	
ID	AAG35776 standard; Protein; 501 AA.
XX	XX
XX	AC AAG35776;
XX	XX
XX	18-OCT-2000 (first entry)
XX	XX
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 43753.
XX	XX Protein identification; signal transduction pathway; metabolic pathway;
KW	KW hybridisation assay; Genetic mapping; Gene expression control; promoter;
KW	KW termination sequence.
XX	XX Arabidopsis thaliana.
OS	OS
PN	PN EP1033405-A2.
XX	XX
PD	PD 06-SEP-2000.
XX	XX
PF	PF 25-FEB-2000; 2000EP-0301439.
XX	XX
PR	PR 25-FEB-1999; 99US-0121825.
PR	PR 03-MAR-1999; 99US-0123180.
PR	PR 03-MAR-1999; 99US-0123548.
PR	PR 23-MAR-1999; 99US-0125788.
PR	PR 25-MAR-1999; 99US-0126264.
PR	PR 29-MAR-1999; 99US-0126785.
PR	PR 01-APR-1999; 99US-0127462.
PR	PR 06-APR-1999; 99US-0128234.
PR	PR 08-APR-1999; 99US-0128714.
PR	PR 18-APR-1999; 99US-0129845.
PR	PR 19-APR-1999; 99US-0130077.
PR	PR 21-APR-1999; 99US-0130449.
PR	PR 23-APR-1999; 99US-0130510.
PR	PR 23-APR-1999; 99US-0130891.
PR	PR 28-APR-1999; 99US-0131449.
PR	PR 30-APR-1999; 99US-0132048.
PR	PR 30-APR-1999; 99US-0132407.
PR	PR 04-MAY-1999; 99US-0132484.
PR	PR 05-MAY-1999; 99US-0132485.
PR	PR 06-MAY-1999; 99US-0132486.
PR	PR 07-MAY-1999; 99US-0132487.
PR	PR 11-MAY-1999; 99US-0132863.
PR	PR 14-MAY-1999; 99US-0134256.
PR	PR 14-MAY-1999; 99US-0134218.
PR	PR 14-MAY-1999; 99US-0134219.
PR	PR 14-MAY-1999; 99US-0134221.
PR	PR 14-MAY-1999; 99US-0134370.
PR	PR 18-MAY-1999; 99US-0134768.
PR	PR 19-MAY-1999; 99US-0134941.
PR	PR 20-MAY-1999; 99US-0135124.
PR	PR 21-MAY-1999; 99US-0135353.
PR	PR 25-MAY-1999; 99US-0135629.
PR	PR 25-MAY-1999; 99US-0136021.
PR	PR 27-MAY-1999; 99US-0136392.
PR	PR 28-MAY-1999; 99US-0136782.
PR	PR 01-JUN-1999; 99US-0137422.
PR	PR 03-JUN-1999; 99US-0137528.
PR	PR 04-JUN-1999; 99US-0137502.
PR	PR 07-JUN-1999; 99US-0137724.
PR	PR 08-JUN-1999; 99US-0138094.
PR	PR 10-JUN-1999; 99US-0138540.
PR	PR 10-JUN-1999; 99US-0138847.
PR	PR 14-JUN-1999; 99US-0139119.
PR	PR 16-JUN-1999; 99US-0139452.
PR	PR 16-JUN-1999; 99US-0139453.
PR	PR 17-JUN-1999; 99US-0139492.
PR	PR 18-JUN-1999; 99US-0139454.
PR	PR 18-JUN-1999; 99US-0139455.
PR	PR 18-JUN-1999; 99US-0139456.
PR	PR 18-JUN-1999; 99US-0139457.

```

PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 28-JUN-1999; 99US-0140891.
PR 30-JUN-1999; 99US-0141267.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143842.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144864.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148664.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.

```

```

PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157753.
PR 07-OCT-1999; 99US-0157865.
PR 08-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158322.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match          94.8%; Score 2458; DB 21; Length 501;
Best Local Similarity 94.8%; Pred. No. 2.2e-210;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 4 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGOFGTTYLCTEKSTSANACKSIKPKLV 63
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 KPNRRPSNSVLPYETPLRLRDHYLLGKLGQGOFGTTYLCTEKSSSANACKSIKPKLV 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 64 CREDYEDVWREIQIMHLSHPNVRKGTYESVVFHVWMEVCEGGEFLDRIVSKGHS 123
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 CREDYEDVWREIQIMHLSHPNVRKGTYESVVFHVWMEVCEGGEFLDRIVSKGCS 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 124 EREAUKLIKILGWACHSLGWNHRDLKPNFLPDSPKDDAKLKATDFGLSVFYKPGQY 183
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 123 EREAUKLIKILGWACHSLGWNHRDLKPNFLPDSPKDDAKLKATDFGLSVFYKPGQY 182
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

QY 184 LYDVVGSPPYVAPVLLKCYGPEIDVMSAGVILLYILLSGVPEPWATESGIFRQILQGLK 243  
DB 183 LYDVVGSPPYVAPVLLKCYGPEIDVMSAGVILLYILLSGVPEPWATESGIFRQILQGLK 242  
QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL 303  
DB 243 DFKSDPWPPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEHAAPDKPLDPAVLSRL 302  
QY 304 KQFSQMKIKQWALRVIAERLSEEEIGGLKELFKMIDTNSGTTITEELKAGLKRYSSEL 363  
DB 303 KQFSQMKIKQWALRVIAERLSEEEIGGLKELFKMIDTNSGTTITEELKAGLKRYSSEL 362  
QY 364 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAAFSDFDKDGSGYITIDE 423  
DB 363 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAAFSDFDKDGSGYITIDE 422  
QY 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMRKGDGVGSRRTMKNLNFNIA 483  
DB 423 LOQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMRKGDGVGSRRTMKNLNFNIA 482  
QY 484 DAFGVDG----EKSD 495  
DB 483 EAFGVEDTSSTAKSD 498  
RESULT 3  
ID AAM48001 standard; Protein; 501 AA.  
AC AAM48001;  
XX 08-MAR-2002 (first entry)  
XX Arabidopsis CDPK4 SEQ ID NO 3.  
KW Arabidopsis; CDPK4; calcium dependent protein kinase; oilseed;  
KW disease resistance; agricultural; pathogen; crop yield; ornamental;  
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;  
KW transgenic; plant; enzyme.  
XX Arabidopsis thaliana.  
XX WO200184911-A1.  
XX 15-NOV-2001.  
XX 04-MAY-2001; 2001WO-US14368.  
XX 05-MAY-2000; 2000US-201925P.  
XX (GEO) GEN HOSPITAL CORP.  
XX Sheen J;  
XX WPI; 2002-062179/08.  
XX N-PSDB; ABA06022.  
XX Producing plant having increased disease resistance, comprises  
XX regenerating plant from a non-naturally occurring plant cell  
XX over-expressing a polynucleotide encoding a calcium dependent protein  
XX kinase polypeptide -  
XX Disclosure; Fig 2; 44pp; English.  
XX The invention relates to producing a plant having increased disease  
XX resistance, comprising providing a non-naturally occurring plant cell  
XX over-expressing a polynucleotide encoding a calcium dependent protein  
XX kinase (CDPK) polypeptide and regenerating a plant from the plant  
XX cell, where the CDPK polypeptide is expressed in the plant, increasing  
XX the resistance of the plant to disease as compared to a naturally-  
XX occurring plant. The method is useful for a variety of  
XX agricultural and commercial purposes including improving a plant's

CC resistance against plant pathogens, increasing crop yields, improving  
CC crop and ornamental quality and reducing agricultural production costs.  
CC The method facilitates an effective and economical method for in-plant  
CC protection against plant pathogen, reducing or minimizing the need for  
CC traditional chemical practices (e.g. application of fungicides,  
CC bactericides, nematocides, insecticides, or viricides) that are typically  
CC used by farmers for controlling the spread of plant pathogens and  
CC providing protection against disease causing pathogens. The method  
CC contributes to the production of high quality and high yield agricultural  
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
CC having reduced spots, blemishes and blotches that are caused by  
CC pathogens, agricultural products with increased shelf-life and reduced  
CC handling costs and high quality and yield crops for agricultural  
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
CC thaliana CDPK4 of the invention.  
XX  
SQ Sequence 501 AA;  
Query Match 34.8%; Score 2458; DB 23; Length 501;  
Best Local Similarity 34.8%; Pred. NO. 2.2e-210;  
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;  
QY 4 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPKRKLIV 63  
DB 3 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPKRKLIV 62  
QY 64 CREDYEDVWREIQIMHLSSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSGHFS 123  
DB 63 CREDYEDVWREIQIMHLSSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSGHFS 122  
QY 124 EREAVKLIKTLGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQY 183  
DB 123 EREAVKLIKTLGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQY 182  
QY 184 LYDVVGSPPYVAPVLLKCYGPEIDVMSAGVILLYILLSGVPEPWATESGIFRQILQGLK 243  
DB 183 LYDVVGSPPYVAPVLLKCYGPEIDVMSAGVILLYILLSGVPEPWATESGIFRQILQGLK 242  
QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL 303  
DB 243 DFKSDPWPPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEHAAPDKPLDPAVLSRL 302  
QY 304 KQFSQMKIKQWALRVIAERLSEEEIGGLKELFKMIDTNSGTTITEELKAGLKRYSSEL 363  
DB 303 KQFSQMKIKQWALRVIAERLSEEEIGGLKELFKMIDTNSGTTITEELKAGLKRYSSEL 362  
QY 364 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAAFSDFDKDGSGYITIDE 423  
DB 363 MESEIKSLMDAADINSGTIDYGEFLAATLHMKNVREELVAAFSDFDKDGSGYITIDE 422  
QY 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMRKGDGVGSRRTMKNLNFNIA 483  
DB 423 LOQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMRKGDGVGSRRTMKNLNFNIA 482  
QY 484 DAFGVDG----EKSD 495  
DB 483 EAFGVEDTSSTAKSD 498  
RESULT 4  
ID AAG35777 standard; Protein; 425 AA.  
XX AAG35777;  
XX 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 43754.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

[illegible]

PR	13-SEP-1999;	99US-0153758.	
PR	15-SEP-1999;	99US-0154018.	
PR	16-SEP-1999;	99US-0154039.	
PR	20-SEP-1999;	99US-0154779.	
PR	22-SEP-1999;	99US-0155139.	
PR	23-SEP-1999;	99US-0155486.	
PR	24-SEP-1999;	99US-0155659.	
PR	28-SEP-1999;	99US-0156458.	
PR	29-SEP-1999;	99US-0156596.	
PR	04-OCT-1999;	99US-0157117.	
PR	05-OCT-1999;	99US-0157753.	
PR	06-OCT-1999;	99US-0157865.	
PR	07-OCT-1999;	99US-0158029.	
PR	08-OCT-1999;	99US-0158232.	
PR	12-OCT-1999;	99US-0158369.	
PR	13-OCT-1999;	99US-0159293.	
PR	13-OCT-1999;	99US-0159294.	
PR	13-OCT-1999;	99US-0159295.	
PR	14-OCT-1999;	99US-0159329.	
PR	14-OCT-1999;	99US-0159330.	
PR	14-OCT-1999;	99US-0159331.	
PR	14-OCT-1999;	99US-0159637.	
PR	14-OCT-1999;	99US-0159638.	
PR	18-OCT-1999;	99US-0159584.	
PR	21-OCT-1999;	99US-0160741.	
PR	21-OCT-1999;	99US-0160767.	
PR	21-OCT-1999;	99US-0160768.	
PR	21-OCT-1999;	99US-0160770.	
PR	21-OCT-1999;	99US-0160814.	
PR	21-OCT-1999;	99US-0160815.	
PR	22-OCT-1999;	99US-0160980.	
PR	22-OCT-1999;	99US-0160981.	
PR	22-OCT-1999;	99US-0160989.	
PR	25-OCT-1999;	99US-0161404.	
PR	25-OCT-1999;	99US-0161405.	
PR	25-OCT-1999;	99US-0161406.	
PR	26-OCT-1999;	99US-0161359.	
PR	26-OCT-1999;	99US-0161360.	
PR	26-OCT-1999;	99US-0161361.	
PR	28-OCT-1999;	99US-0161920.	
PR	28-OCT-1999;	99US-0161992.	
PR	28-OCT-1999;	99US-0161993.	
PR	29-OCT-1999;	99US-0162142.	
Query Match 79.6%; Score 2064; DB 21; Length 425;			
Best Local Similarity 94.5%; Pred. No. 2.4e-175;			
Matches 399; Conservative 6; Mismatches 13; Indels 4; Gaps 1;			
QY	78	MHLSEHPNVRIKGYEDSVFVHIVMEYCEGGELFDRIVSKGHFSEREAVKLKLTILGV	137
DB	1	MHLSEHPNVRIKGYEDSVFVHIVMEYCEGGELFDRIVSKGFSEREAAKLKLTILGV	60
QY	138	VEACHSLGWHRLKPENFLFDSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYVAPE	197
DB	61	VEACHSLGWHRLKPENFLFDSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYVAPE	120
QY	198	VLKXCVGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDKPSDPWPTISEAA	257
DB	121	VLKXCVGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDKPSDPWPTISEGA	180
QY	258	KDLIYKMLSPKRSIAEHALCHPMIVDEQAAPDKPLDPAVLISLKFQSQNKIKKVAL	317
DB	181	KDLIYKMLDRSPKRSIAEHALCHPMIVDEHAAPDKPLDPAVLISLKFQSQNKIKKVAL	240
QY	318	RVTARLSSEIEGLKELFKWIDTNSGITTPPEELKAGLKRVGSELMSEIKSLMDAADI	377
DB	241	RVTARLSSEIEGLKELFKWIDTNSGITTPPEELKAGLKRVGSELMSEIKSLMDAADI	300
QY	378	DNSTIDYGEFLAATLHMNKNREBILVAFSPDKDGSYITIDELQACTEFGLCDETP	437
DB	301	DNSTIDYGEFLAATLHMNKNREBILVAFSPDKDGSYITIDELQACTEFGLCDETP	360
QY	438	LDDMIKEIDLNDGKIDFSEFTAMMKGGVGRSRTMRNLFNFIABFVDETSSTAKS	420

Query Match		74.5%;	Score 1932;	DB 20;	Length 512;
Best Local Similarity		77.1%;	Pred. No. 1.9e-163;		
Matches 370;		Conservative 51;	Mismatches 51;	Indels 8;	Gaps 4;
QY	14	VLVQTPRLRDHYLLGKLGQGGTGYTCTEKTSTANYACKSIKPKKLVCREDYEDVWR	73		
DB	22	VLVQTNREVVEVRKLGQGGTGTCTCTRRASGGKFAKSIKPKKLCKEDYEDVWR	81		
QY	74	EIQIMHLSHPNVVTKIGTYEDSVFVHIVMEVCEGGLFDRIIVSKGHFSREAVKLIKT	133		
DB	82	EIQIMHLSHANVRIEGTYEDSTAVHIVMLCEGGLFDRIIVQGHYSERQAAELIKT	141		
QY	134	ILGVVEACHSLGVMHRLKPNFLDPSKDDAKLATDGLSVFYKPGQYLYDVWGSPYY	193		
DB	142	IVVVEACHSLGVMHRLKPNFLFDITDEDAKLATDGLSVFYKPGESFCDVWGSPYY	201		
QY	194	VAPEVLKCCVGPBEIDVMSAGVILYIILSGVPPFWAETESGIFRQILQKGLDFKSDPWTI	253		
DB	202	VAPEVLKLYGPESDVMSAGVILYIILSGVPPFWAETESGIFRQILGLKDFHSEFPWSI	261		
QY	254	SEAAKDILYKWLSPKRTISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSQMNKIK	313		
DB	262	SDSANDILRKWLQONPKTRLTAEVLRHFWIVDDNIADPKLDSAVLSRLKQFSAMNKIK	321		
QY	314	KMALRVIAERLSEEEIGGLKELFKMIDTNSGTITTFE-----LKAGLKVGVSELMSEIK	369		
DB	322	KMALRVIAERLSEEEIGGLKELFKMIDTNSGTITTFDELKDGLKDKLKVGVSELMSEIK	381		
QY	370	SLMDAADINSGTIDYGEFLAATLHNMKWEREILVAAPSDPKDQSGYITIDELQSACT	429		
DB	382	DLMDAADINSGTIDYGEFLAATVHLNKLEENLVSAFSDPKDQSGYITIDELQACK	441		
QY	430	EFGLCDTPELDMIKEIDLNDGKIDFSEFTAMVRKGD-GVGRSRTMMKNLNFNIADAFGV	488		
DB	442	DFGLDDIHIDMIKEIDQDNDGQIDYGEFAAMVRKNGGIGR-RTMRKTL--NLRDALGL	498		
RESULT 6					
AAG35778					
ID	AAG35778 standard; Protein; 399 AA.				
XX	AAG35778;				
AC					
XX					
DT	18-OCT-2000 (first entry)				
DE					
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 43755.				
XX	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
KW	termination sequence.				
XX	Arabidopsis thaliana.				
OS					
PN	EP1033405-A2.				
XX					
PD	06-SEP-2000.				
XX					
PF	25-FEB-2000; 2000EP-0301439.				
XX					
PR	25-FEB-1999; 99US-0121825.				
PR	05-MAR-1999; 99US-0123180.				
PR	09-MAR-1999; 99US-0123548.				
PR	23-MAR-1999; 99US-0125788.				
PR	25-MAR-1999; 99US-0126264.				
PR	29-MAR-1999; 99US-0126785.				
PR	01-APR-1999; 99US-0127462.				
PR	06-APR-1999; 99US-0128234.				
PR	08-APR-1999; 99US-0128714.				
PR	16-APR-1999; 99US-0129845.				
PR	19-APR-1999; 99US-0130077.				
PR	21-APR-1999; 99US-0130449.				
PR	23-APR-1999; 99US-0130510.				
PR	23-APR-1999; 99US-0130891.				

PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135623.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	03-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144684.



XX	25-FEB-2000; 2000EP-0301439.	PR	08-JUL-1999;	99US-0142803.
PF		PR	09-JUL-1999;	99US-0142920.
XX		PR	12-JUL-1999;	99US-0142977.
XX		PR	13-JUL-1999;	99US-0143542.
PR	25-FEB-1999;	PR	14-JUL-1999;	99US-0143624.
PR	05-MAR-1999;	PR	15-JUL-1999;	99US-0144005.
PR	09-MAR-1999;	PR	16-JUL-1999;	99US-0144085.
PR	23-MAR-1999;	PR	16-JUL-1999;	99US-0144086.
PR	25-MAR-1999;	PR	19-JUL-1999;	99US-0144325.
PR	29-MAR-1999;	PR	19-JUL-1999;	99US-0144331.
PR	01-APR-1999;	PR	19-JUL-1999;	99US-0144332.
PR	08-APR-1999;	PR	19-JUL-1999;	99US-0144333.
PR	08-APR-1999;	PR	19-JUL-1999;	99US-0144334.
PR	16-APR-1999;	PR	19-JUL-1999;	99US-0144335.
PR	19-APR-1999;	PR	20-JUL-1999;	99US-0144352.
PR	21-APR-1999;	PR	20-JUL-1999;	99US-0144632.
PR	23-APR-1999;	PR	20-JUL-1999;	99US-0144884.
PR	28-APR-1999;	PR	21-JUL-1999;	99US-0144814.
PR	28-APR-1999;	PR	21-JUL-1999;	99US-0145086.
PR	30-APR-1999;	PR	21-JUL-1999;	99US-0145088.
PR	30-APR-1999;	PR	21-JUL-1999;	99US-0145089.
PR	04-MAY-1999;	PR	22-JUL-1999;	99US-0145087.
PR	05-MAY-1999;	PR	22-JUL-1999;	99US-0145089.
PR	06-MAY-1999;	PR	22-JUL-1999;	99US-0145192.
PR	06-MAY-1999;	PR	23-JUL-1999;	99US-0145145.
PR	07-MAY-1999;	PR	23-JUL-1999;	99US-0145218.
PR	11-MAY-1999;	PR	23-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	PR	27-JUL-1999;	99US-0145918.
PR	14-MAY-1999;	PR	27-JUL-1999;	99US-0145919.
PR	18-MAY-1999;	PR	28-JUL-1999;	99US-0145951.
PR	19-MAY-1999;	PR	28-JUL-1999;	99US-0145951.
PR	20-MAY-1999;	PR	02-AUG-1999;	99US-0146386.
PR	21-MAY-1999;	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	PR	02-AUG-1999;	99US-0146389.
PR	24-MAY-1999;	PR	02-AUG-1999;	99US-0147038.
PR	25-MAY-1999;	PR	04-AUG-1999;	99US-0147204.
PR	27-MAY-1999;	PR	04-AUG-1999;	99US-0147302.
PR	28-MAY-1999;	PR	05-AUG-1999;	99US-0147192.
PR	01-JUN-1999;	PR	05-AUG-1999;	99US-0147260.
PR	03-JUN-1999;	PR	06-AUG-1999;	99US-0147303.
PR	04-JUN-1999;	PR	06-AUG-1999;	99US-0147416.
PR	07-JUN-1999;	PR	09-AUG-1999;	99US-0147493.
PR	08-JUN-1999;	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	PR	12-AUG-1999;	99US-0148241.
PR	16-JUN-1999;	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	PR	30-AUG-1999;	99US-0151303.
PR	22-JUN-1999;	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	PR	01-SEP-1999;	99US-0151930.
PR	23-JUN-1999;	PR	07-SEP-1999;	99US-0152363.
PR	24-JUN-1999;	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	PR	23-SEP-1999;	99US-0155486.

PR	24-SEP-1999;	99US-01556559.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160988.
PR	22-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	26-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161932.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 67.2%; Score 1742; DB 21; Length 483;		
Best Local Similarity 68.4%; Pred. No. 1.5e-146;		
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;		
QY	6	NPRRSENTPVQTPRLRDHYLGHKLGQGGFTTYICTKSTANTYACKSIKRLKLCR 65
DB	4	NPDNQAYVYLGHTNIRDIVTLRSKLGQGGFTTYLCTEIASGVYACKSIKRLKLSK 63
QY	66	EYEDVWREIQIWMHLSHPNVVRIKGYEDSVFVHVEYCEGGEFLDRIVSKGHFSES 125
DB	64	EVEDVRRRIQIWMHLSHAGSVITIKGYEDSVFVHVEYCEGGEFLDRIVSKGHFSES 123
QY	126	EAVKLIKTLGVVEACHSLGVNMRDLKPNFLFDSKDDAKLKTDFGLSVFYKPGQYLY 185
DB	124	KAELTKIIVGVVEACHSLGVNMRDLKPNFLFVNNKDDDFSLKAIDFGLSVFYKPGQY 183
QY	186	DVVGSPYVAPVKKVCGPETDVMSAGVILYLLSGVPPWAEETSGIPRQILQGLDF 245
DB	184	DVVGSPYVAPVKKVCGPETDVMSAGVILYLLSGVPPWAEETSGIPRQILQGLDF 243
QY	246	KSDPWPTEISAAKDLIYKMLERSPKKRISAHEALCHPVIWVQAPKPLDPVLSRLKQ 305
DB	244	ESDPWEVSDSAXDLIRMLSSKPAERLTAHEVLRHPICENGVAIPDPAVLSRLKQ 303
QY	306	FSQWNIKKVALVIAERLSEEEIGLKFEMIDTDSGTTTPEELKAGLKVYGSSELM 365
DB	304	FSQWNIKKVALVIAERLSEEEIGLKFEMIDTDSGTTTPEELKAGLKVYGSSELM 363
QY	366	SEIKSLMDADIQNSGTIDYGEFLAATLHMNKREREELIVAAFSDFDKDGGYITIDELQ 425
DB	364	TEHDLMDADVNSGTIDYSEFIATIHNLKREHVLVAAFQVFDKDGSGFTIDELQ 423
QY	426	SACTEFLGCTPDDWIKEDLDNDGKIDFSEFTAMRKGD-GVGRSRMTMKNFNFIAD:484
DB	424	QACVEHGMADVFLIEDIKEDVQNDGKIDYGEFVEMVQKGNAGVGR-RTMNRSLNISM 482

QY	485 A 485
DB	483 A 483
RESULT 8	
ID	AAG31157 standard; Protein; 556 AA.
XX	AAG31157;
AC	AAG31157;
XX	17-OCT-2000 (first entry)
DT	XX
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 37371.
XX	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	Arabidopsis thaliana.
OS	Arabidopsis thaliana.
XX	EP1033405-A2.
PN	06-SEP-2000.
PD	25-FEB-2000; 2000EP-0301439.
PF	XX
XX	25-FEB-1999; 99US-0121825.
XX	05-MAR-1999; 99US-012180.
PR	03-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	23-APR-1999; 99US-0130891.
PR	28-APR-1999; 99US-0131449.
PR	30-APR-1999; 99US-0132048.
PR	30-APR-1999; 99US-0132407.
PR	04-MAY-1999; 99US-0132484.
PR	05-MAY-1999; 99US-0132485.
PR	06-MAY-1999; 99US-0132486.
PR	07-MAY-1999; 99US-0132487.
PR	11-MAY-1999; 99US-0134256.
PR	14-MAY-1999; 99US-0134219.
PR	14-MAY-1999; 99US-0134221.
PR	14-MAY-1999; 99US-0134370.
PR	18-MAY-1999; 99US-0134768.
PR	19-MAY-1999; 99US-0134941.
PR	20-MAY-1999; 99US-0135124.
PR	21-MAY-1999; 99US-0135353.
PR	24-MAY-1999; 99US-0135629.
PR	25-MAY-1999; 99US-0136021.
PR	27-MAY-1999; 99US-0136392.
PR	28-MAY-1999; 99US-0136782.
PR	01-JUN-1999; 99US-0137222.
PR	03-JUN-1999; 99US-0137528.
PR	04-JUN-1999; 99US-0137502.
PR	07-JUN-1999; 99US-0137724.
PR	08-JUN-1999; 99US-0138094.
PR	10-JUN-1999; 99US-0138540.
PR	10-JUN-1999; 99US-0138847.
PR	14-JUN-1999; 99US-0139119.
PR	16-JUN-1999; 99US-0139452.
PR	16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.  
 PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.  
 PR 18-JUN-1999; 99US-0139460.  
 PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 22-JUN-1999; 99US-0139899.  
 PR 23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 23-JUN-1999; 99US-0140695.  
 PR 28-JUN-1999; 99US-0140823.  
 PR 28-JUN-1999; 99US-0140991.  
 PR 30-JUN-1999; 99US-0141287.  
 PR 01-JUL-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142803.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 18-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 19-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 23-JUL-1999; 99US-0145192.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 23-JUL-1999; 99US-0145219.  
 PR 23-JUL-1999; 99US-0145224.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 27-JUL-1999; 99US-0145919.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 02-AUG-1999; 99US-0146389.  
 PR 03-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 05-AUG-1999; 99US-0147960.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 09-AUG-1999; 99US-0147935.  
 PR 10-AUG-1999; 99US-0148171.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.

PR 13-AUG-1999; 99US-0148684.  
 PR 16-AUG-1999; 99US-0149368.  
 PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149446.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 16-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 22-OCT-1999; 99US-0161404.  
 PR 23-OCT-1999; 99US-0161405.  
 PR 23-OCT-1999; 99US-0161406.  
 PR 25-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161922.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 67.2%; Score 1742; DB 21; Length 556;  
 Best Local Similarity 68.4%; Pred. No. 1.9e-146;  
 Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;  
 QY 6 NPPRPSTVLPYOTPLRDRHYLLGKLGQGGTGYLCTEKSTSNYACKSIPKPKLYCR 65  
 DB 77 NPDNQAYVVLGHGTPNIRDIYTLRSKLGQGGTGYLCTEIASGVYACKSISKKLISK 136  
 QY 66 EDYEDYWRREIQIWHLHSEHPNVRIKGTYESDVFVHIVMEVCEGCELFDRIVSKGHFSER 125



PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0145386.  
PR 02-AUG-1999; 99US-0143388.  
PR 02-AUG-1999; 99US-0143389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149829.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 10-SEP-1999; 99US-0152363.  
PR 13-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.

PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 65.7%; Score 1703; DB 21; Length 856;  
Best Local Similarity 65.7%; Pred. No. 1e-142;  
Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;

QY 2 ETKPNRRP-----SNTVLPYQTPRLADHVLGKLGQGGQFGTTLCTEKSTS 49  
DB 348 ETKAEPQKPKHMRVSSAGLRTESVLQKRTENKFEYSLGRKLGQGGQFGTTLCLKGTG 407  
QY 50 ANYACKSIPKRLVCREDYEDVWREIQIMHLSHPNVVRIKGYEDSVFVHIVNEVCEG 109  
DB 408 NEYACKSISKRKLLTDEDVEDVREIQIMHLSHPNVISIKGAYEDVVAHVLNMLCSG 467  
QY 110 GELPDRIVSKGHFSEREAVKLKTLGVVEACHSIGVWHRDLKPNFLFDSFKDADAKLA 169  
DB 468 GELFDRIIQORHYTERKAELARTIVGLEACHSLGVWHRDLKPNFLFVSREDSLLKT 527  
QY 170 TDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCKYGPEDVMSAGVILYLLSGVPPFWA- 228  
DB 528 IDFGLSNFFKPDVEFTDVVGSPPYVAPEVLKRYGPESDVMSAGVIVVILLSGVPPFWAG 587  
QY 229 -----ETESGIFRQILOGKLDPKSDPWTISAAKDLIKMLERSPKKXISAHE 277  
DB 588 SEYNLFMSKYTEQGIPEQVLUHGLDFSSDPWPSISESAKDLVKRMLVRDPKRLIDAHQ 647  
QY 278 ALCHPMIVDEQAAPDKPLDPAYLSRLKQFSQNMKIKKQALRVIAERLSEEEIGGKELFK 337  
DB 648 VLCHPNVQIDGVAPDKPLDSAVLSRMKQFSANMKFKKVALAVIAESLSEEEIAGLKQMKF 707  
QY 338 MIDTNSGTTFEELKAGLKRVGSELMSEIKSLMDAADIDNSGTTIDYGEFLAATLHNK 397  
DB 708 MIDADNSGQITFEELKAGLKRVGANLKESEILDLMQAADVDNSGTTIDYKEFTAATLHNK 767  
QY 398 MEREEILVAAFSDPKDGSYITIDELQACTEFGLCDPLDDMIKEIDLNDGKIDFSE 457  
DB 768 IEREDHLFAAFSYFDKDESGFITPDELOQACEFGEVDARIEEMVRDQDKDGRIDYNE 827  
QY 458 FTAMMRKGDGVG 469  
DB 828 FVAMMQKGSIMG 839

RESULT 10  
AAG38598  
ID AAG38598 standard; Protein; 893 AA.  
XX AAG38598;  
AC  
XX  
XX 18-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 47641.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS  
XX  
XX EP1033405-A2.







QY 50 ANYACKSIKPKLVCREDEYVYREIQIMHLSHPNVVRIKGTVEDGVFVHVMVEVCEG 109  
Db 569 NEVACKSISKKLLTDEVEDVREIQIMHLAGPNVISIKGAYEDVVAHLVYELCSG 628  
QY 110 GELFDRIYVKGHSEAEVAVLKITLGVVVEACHSLGWHRDLKPNFLDFSPKDDAKKA 169  
Db 629 GELFDRIYVKGHSEAEVAVLKITLGVVVEACHSLGWHRDLKPNFLDFVSRDEESLLKT 688  
QY 170 TDFGLSVFYKPGGYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWA- 228  
Db 689 IDFGLSWFFKPPDVFDDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAG 748  
QY 229 -----ETESGIFRQILQGLKDFKSDPWTISEAAKOLIYXMLERSPKRISAE 277  
Db 749 SEVNLFSMKYTETEQIGFEQVLHGDLDFFSDPWSSESAXDLVRKMLVROPKRLTAHQ 808  
QY 278 ALCHPWIVDQAPDPLDPAVLRSRKQSONKIKKALRVIAERLSEEBTGGKLEFK 337  
Db 809 VLCHPWVQIDGVAPDPLDPAVLRSRKQSONKIKKALRVIAERLSEEBTGGKLEFK 337  
QY 338 MIDTNSGTTTFEELKAGLRKVGSELMESEIKSLMDAADINDSGTIDYGEFLAATLHMK 397  
Db 869 MIDADNSGTTTFEELKAGLRKVGSELMESEIKSLMDAADINDSGTIDYGEFLAATLHMK 928  
QY 398 MERBEILVAAPSPDFKDGSGYITIDELQACTEFGCLDPLDDMIKEIDLNDGKIDFSE 457  
Db 929 IEREDHLLFAAFSYFDKDSGFTIPDELQACSEFGVEDARIBEMMRDVEDVDQDKGRIDYNE 988  
QY 458 FTAMWRKGDGVG 469  
Db 989 FVAMVQKGSIMG 1000  
RESULT 12  
AAM52842  
ID AAM52842 standard; Protein; 549 AA.  
XX  
AC AAM52842;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Physcomitrella patens CPK-2 protein, SEQ ID NO:39.  
XX  
KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;  
KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;  
KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;  
KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;  
KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;  
KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;  
KW calcium-dependent protein kinase-2; CPK-2; overexpression;  
KW environmental stress; salinity; drought; temperature; tolerance;  
KW transgenic plant; EST; expressed sequence tag.  
XX  
OS Physcomitrella patens.  
XX  
FN WO200177356-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-US11435.  
XX  
PR 07-APR-2000; 2000US-196001P.  
XX  
XX (BADI ) BASF PLANT SCI GMBH.  
XX  
PI Da Costa Silva EO, Bohnert HJ, Van Thielens N, Chen R;  
PI Sarria-Millan R;  
XX WPI; 2002-049153/06.  
DR N-PSDB; ABA91081.  
XX  
PT New protein, useful for increasing tolerance to environmental stress,  
PT comprises a Protein Kinase Stress-Related Protein selected from

PT Protein kinases, Casein kinase homologs, MAP kinases or Calcium  
PT dependent protein kinases  
XX  
PS Claim 13; Fig 3M; 154pp; English.  
XX  
CC Sequences AAM52830-AAM52842 represent novel protein kinase stress-related  
CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences  
CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA  
CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-  
CC ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs  
CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7  
CC (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase  
CC homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase  
CC homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),  
CC MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),  
CC calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein  
CC kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer  
CC tolerance to environmental stresses such as salinity, drought,  
CC temperature, metal, chemical, pathogenic and oxidative stress.  
CC Physcomitrella patens PKSRP nucleic acids may be used to generate  
CC transgenic plants and seeds with increased tolerance to salinity, drought  
CC and temperature. The transgenic plants generated can be monocots or  
CC dicots and are especially maize, wheat, rice, oat, triticale, rice,  
CC barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants  
CC (e.g., soybean, peanut, Vicia species, alfalfa), solanaceous plants  
CC (e.g., potato, tobacco, auhergine, pepper, tomato), coffee, cacao, tea,  
CC Salix species, oil palm, coconut, perennial grasses and forage crops. The  
CC PKSRP nucleotide and proteins may also be used in evolutionary and  
CC protein structural studies and as markers for specific regions of  
CC the genome.  
XX  
SQ Sequence 549 AA;  
Query Match 58.2%; Score 1509.5; DB 23; Length 549;  
Best Local Similarity 60.8%; Pred. No. 9.9e-126;  
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;  
QY 5 PNPRLPSNT---VLPYQTPRLDRHYLLKGLKGGQGGTTLCTEKTSTANYACKSIKRX 61  
Db 69 PRPKPASRSVSGVLGKPLSDIRQSYILGRELGGQGGTTLCTDQMTNEAYACKSIKRX 128  
QY 62 LVCREDEYVREIQIMHLSHPNVVRIKGTVEDGVFVHVMVEVCEGELFDRIYVSKGH 121  
Db 129 LTSKEIDYKREVQIMHLSGTPNIIVLKDVFEDKSHVLMELCAGGELFDRIYVSKGH 189  
QY 122 FSRREAVKLITLGVVVEACHSLGVHRLKPNFLDFSPKDDAKKATDFGLSVFYKPG 181  
Db 189 YSERRAADMCRLVNVVHCHSLGVHRLKPNFLDFSKAEDAPLKATDFGLSTFFKPG 248  
QY 182 QYLYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 241  
Db 249 DVFDIVGSAYVVAPEVLKRSYGPEADVWSAGVIVVILLCGVPPFWAETEQGIFDAVLKG 308  
QY 242 KLDPKSDPWPPTISEAAKDLIYXMLESPKRISEAEALCHPWIVDEQAAPDKPLDPAVL 301  
Db 309 HIDPNDPWPXINGAKDLVRKMLNPNVKIRLTAQVNLNHPMKEDGADPVDLNAVLT 368  
QY 302 RLKQFSQMNKIKKVALRVIAERLSEEBTGGKLEFLAATLHMKWEREELVAAPSDFDKDGSGYITI 361  
Db 369 RLKNFSAANKMKKALKVIAESLSEEBTGGKLEFLAATLHMKWEREELVAAPSDFDKDGSGYITI 428  
QY 362 ELMESEIKSLMDAADINDSGTIDYGEFLAATLHMKWEREELVAAPSDFDKDGSGYITI 421  
Db 429 KLANESDIRKLEAAADVGNKIDFNFIATMNMNTEKEDHLMAAFMFDINDSGYITI 488  
QY 422 DELQACTEFGCLD-TPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476  
Db 489 DELQAEKMGMDGPETIQEIISEVTDNDGRIDYDEFVAMMRKGNPGAENGTTVKNK 545  
RESULT 13  
AAG31159  
ID AAG31159 standard; Protein; 408 AA.

XX AC ARG31159;  
XX AC  
XX DT 17-OCT-2000 (first entry)  
XX DE  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 37373.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX XX  
XX PR 25-FEB-1999; 99US-0121825.  
XX PR 05-MAR-1999; 99US-0123180.  
XX PR 09-MAR-1999; 99US-0123548.  
XX PR 23-MAR-1999; 99US-0125788.  
XX PR 25-MAR-1999; 99US-0126264.  
XX PR 29-MAR-1999; 99US-0126785.  
XX PR 01-APR-1999; 99US-0127462.  
XX PR 06-APR-1999; 99US-0128234.  
XX PR 08-APR-1999; 99US-0128714.  
XX PR 16-APR-1999; 99US-0129845.  
XX PR 19-APR-1999; 99US-0130077.  
XX PR 21-APR-1999; 99US-0130549.  
XX PR 23-APR-1999; 99US-0130510.  
XX PR 23-APR-1999; 99US-0130891.  
XX PR 28-APR-1999; 99US-0131449.  
XX PR 30-APR-1999; 99US-0132048.  
XX PR 30-APR-1999; 99US-0132407.  
XX PR 04-MAY-1999; 99US-0132484.  
XX PR 05-MAY-1999; 99US-0132485.  
XX PR 06-MAY-1999; 99US-0132486.  
XX PR 06-MAY-1999; 99US-0132487.  
XX PR 07-MAY-1999; 99US-0132863.  
XX PR 11-MAY-1999; 99US-0134256.  
XX PR 14-MAY-1999; 99US-0134218.  
XX PR 14-MAY-1999; 99US-0134219.  
XX PR 14-MAY-1999; 99US-0134221.  
XX PR 14-MAY-1999; 99US-0134370.  
XX PR 18-MAY-1999; 99US-0134768.  
XX PR 19-MAY-1999; 99US-0134941.  
XX PR 20-MAY-1999; 99US-0135124.  
XX PR 21-MAY-1999; 99US-0135353.  
XX PR 24-MAY-1999; 99US-0135629.  
XX PR 25-MAY-1999; 99US-0136021.  
XX PR 27-MAY-1999; 99US-0136392.  
XX PR 28-MAY-1999; 99US-0136782.  
XX PR 01-JUN-1999; 99US-0137222.  
XX PR 03-JUN-1999; 99US-0137528.  
XX PR 04-JUN-1999; 99US-0137502.  
XX PR 07-JUN-1999; 99US-0137724.  
XX PR 08-JUN-1999; 99US-0138094.  
XX PR 10-JUN-1999; 99US-0138540.  
XX PR 10-JUN-1999; 99US-0138847.  
XX PR 14-JUN-1999; 99US-0139119.  
XX PR 16-JUN-1999; 99US-0139452.  
XX PR 16-JUN-1999; 99US-0139453.  
XX PR 17-JUN-1999; 99US-0139492.  
XX PR 18-JUN-1999; 99US-0139454.  
XX PR 18-JUN-1999; 99US-0139455.  
XX PR 18-JUN-1999; 99US-0139456.  
XX PR 18-JUN-1999; 99US-0139457.  
XX PR 18-JUN-1999; 99US-0139458.  
XX PR 18-JUN-1999; 99US-0139459.  
XX PR 18-JUN-1999; 99US-0139460.  
XX PR 18-JUN-1999; 99US-0139461.  
XX PR 18-JUN-1999; 99US-0139462.  
XX PR 18-JUN-1999; 99US-0139463.  
XX PR 18-JUN-1999; 99US-0139464.  
XX PR 21-JUN-1999; 99US-0139763.  
XX PR 21-JUN-1999; 99US-0139817.  
XX PR 22-JUN-1999; 99US-0139899.  
XX PR 23-JUN-1999; 99US-0140353.  
XX PR 23-JUN-1999; 99US-0140354.  
XX PR 24-JUN-1999; 99US-0140695.  
XX PR 28-JUN-1999; 99US-0140823.  
XX PR 29-JUN-1999; 99US-0140991.  
XX PR 30-JUN-1999; 99US-0141287.  
XX PR 01-JUL-1999; 99US-0141842.  
XX PR 01-JUL-1999; 99US-0142154.  
XX PR 02-JUL-1999; 99US-0142055.  
XX PR 06-JUL-1999; 99US-0142390.  
XX PR 08-JUL-1999; 99US-0142803.  
XX PR 09-JUL-1999; 99US-0142920.  
XX PR 12-JUL-1999; 99US-0142977.  
XX PR 13-JUL-1999; 99US-0143542.  
XX PR 14-JUL-1999; 99US-0143624.  
XX PR 15-JUL-1999; 99US-0144005.  
XX PR 15-JUL-1999; 99US-0144085.  
XX PR 16-JUL-1999; 99US-0144086.  
XX PR 18-JUL-1999; 99US-0144325.  
XX PR 18-JUL-1999; 99US-0144331.  
XX PR 19-JUL-1999; 99US-0144332.  
XX PR 19-JUL-1999; 99US-0144333.  
XX PR 19-JUL-1999; 99US-0144334.  
XX PR 19-JUL-1999; 99US-0144335.  
XX PR 20-JUL-1999; 99US-0144632.  
XX PR 20-JUL-1999; 99US-0144884.  
XX PR 21-JUL-1999; 99US-0144814.  
XX PR 21-JUL-1999; 99US-0145086.  
XX PR 21-JUL-1999; 99US-0145088.  
XX PR 22-JUL-1999; 99US-0145089.  
XX PR 22-JUL-1999; 99US-0145087.  
XX PR 23-JUL-1999; 99US-0145192.  
XX PR 23-JUL-1999; 99US-0145145.  
XX PR 23-JUL-1999; 99US-0145218.  
XX PR 23-JUL-1999; 99US-0145224.  
XX PR 26-JUL-1999; 99US-0145276.  
XX PR 27-JUL-1999; 99US-0145913.  
XX PR 27-JUL-1999; 99US-0145918.  
XX PR 27-JUL-1999; 99US-0145919.  
XX PR 28-JUL-1999; 99US-0145951.  
XX PR 02-AUG-1999; 99US-0146385.  
XX PR 02-AUG-1999; 99US-0146388.  
XX PR 02-AUG-1999; 99US-0146389.  
XX PR 03-AUG-1999; 99US-0147038.  
XX PR 04-AUG-1999; 99US-0147204.  
XX PR 04-AUG-1999; 99US-0147302.  
XX PR 05-AUG-1999; 99US-0147192.  
XX PR 05-AUG-1999; 99US-0147260.  
XX PR 06-AUG-1999; 99US-0147303.  
XX PR 06-AUG-1999; 99US-0147415.  
XX PR 08-AUG-1999; 99US-0147493.  
XX PR 09-AUG-1999; 99US-0147935.  
XX PR 10-AUG-1999; 99US-0148171.  
XX PR 11-AUG-1999; 99US-0148319.  
XX PR 12-AUG-1999; 99US-0148341.  
XX PR 13-AUG-1999; 99US-0148565.  
XX PR 13-AUG-1999; 99US-0148684.  
XX PR 16-AUG-1999; 99US-0149368.  
XX PR 17-AUG-1999; 99US-0149175.  
XX PR 18-AUG-1999; 99US-0149425.  
XX PR 20-AUG-1999; 99US-0149722.  
XX PR 20-AUG-1999; 99US-0149723.  
XX PR 20-AUG-1999; 99US-0149923.  
XX PR 23-AUG-1999; 99US-0149902.  
XX PR 23-AUG-1999; 99US-0149930.

PR	25-AUG-1999;	99US-0150566.	
PR	26-AUG-1999;	99US-0150884.	
PR	27-AUG-1999;	99US-0151065.	
PR	27-AUG-1999;	99US-0151066.	
PR	27-AUG-1999;	99US-0151080.	
PR	30-AUG-1999;	99US-0151303.	
PR	31-AUG-1999;	99US-0151438.	
PR	01-SEP-1999;	99US-0151930.	
PR	07-SEP-1999;	99US-0152363.	
PR	10-SEP-1999;	99US-0153070.	
PR	11-SEP-1999;	99US-0153758.	
PR	13-SEP-1999;	99US-0154018.	
PR	15-SEP-1999;	99US-0154039.	
PR	16-SEP-1999;	99US-0154779.	
PR	20-SEP-1999;	99US-0155139.	
PR	22-SEP-1999;	99US-0155486.	
PR	23-SEP-1999;	99US-0155659.	
PR	24-SEP-1999;	99US-0156458.	
PR	28-SEP-1999;	99US-0156596.	
PR	23-SEP-1999;	99US-0157117.	
PR	04-OCT-1999;	99US-0157753.	
PR	05-OCT-1999;	99US-0157865.	
PR	06-OCT-1999;	99US-0158029.	
PR	07-OCT-1999;	99US-0158232.	
PR	08-OCT-1999;	99US-0158369.	
PR	12-OCT-1999;	99US-0159293.	
PR	13-OCT-1999;	99US-0159294.	
PR	13-OCT-1999;	99US-0159295.	
PR	13-OCT-1999;	99US-0159329.	
PR	14-OCT-1999;	99US-0159330.	
PR	14-OCT-1999;	99US-0159331.	
PR	14-OCT-1999;	99US-0159637.	
PR	14-OCT-1999;	99US-0159638.	
PR	18-OCT-1999;	99US-0159584.	
PR	21-OCT-1999;	99US-0160741.	
PR	21-OCT-1999;	99US-0160767.	
PR	21-OCT-1999;	99US-0160768.	
PR	21-OCT-1999;	99US-0160770.	
PR	21-OCT-1999;	99US-0160814.	
PR	21-OCT-1999;	99US-0160815.	
PR	22-OCT-1999;	99US-0160980.	
PR	22-OCT-1999;	99US-0160981.	
PR	22-OCT-1999;	99US-0160989.	
PR	25-OCT-1999;	99US-0161404.	
PR	25-OCT-1999;	99US-0161405.	
PR	25-OCT-1999;	99US-0161406.	
PR	26-OCT-1999;	99US-0161359.	
PR	26-OCT-1999;	99US-0161360.	
PR	26-OCT-1999;	99US-0161361.	
PR	28-OCT-1999;	99US-0161920.	
PR	28-OCT-1999;	99US-0161992.	
PR	28-OCT-1999;	99US-0161993.	
PR	29-OCT-1999;	99US-0162142.	
Query Match 58.2%; Score 1509; DB 21; Length 408;			
Best Local Similarity 69.4%; Pred. No. 7,1e-126;			
Matches 284; Conservative 56; Mismatches 67; Indels 2; Gaps 2;			
QY	78	MHLLSEHENVVRIKGTEDSVFVHIVMEVCEGGELPDRIYVSKGHFSEBAVKLIKTLGV 137	
Db	1	MHLLAGHSIVTIKGAEDSLYVHIVMELCAGGELPDRIIQRGHYSERKAAELTKIIVG 60	
QY	138	VEACHSLGVHRLDKPENFLPDSPKDAKLKATDFGLSVFYKPGQVLYDVWGSPPYVAPE 197	
Db	61	VEACHSLGVHRLDKPENFLVNVKDDFSLKATDFGLSVFFKPGQIFTDVWGSPPYVAPE 120	
QY	198	VLKCYGPEIDVWAGVLYLLSGVPPFWAETESGIFROILOGKLDKSDPWPVTISEAA 257	
Db	121	VLLKRYGPEADVWAGVLYLLSGVPPFWAETQQGIFDAVLKGYIDFSDPWPVLSDSA 180	
QY	258	KDLIYKMLERSPKKRIISAHEALCHPWIDEOAAPDKPLDPAVLSRLKQFSQNNKIKMAL 217	
Db	181	KDLIRMLSSKPAERLTAHEVLRHPWICENGVAIDRALDPAVLISRLKQFSAMNKLKMAL 240	

QY	318	RVIAERLSEEEIGGLKELFKMIDTNSQITIFELKAGLRKVGSELMESEIKSLMDAADI 377	
Db	241	KVIAESLSEEEIAGLRKEMFQAMDTNSGAIITFDELKAGLRKYGSTLKDTEIHDLMDAADV 300	
QY	378	DNSGTIDYGEFLAATLHNKMKREBEILVAAISDFDKDQSGYITIDELQSACTEGLCDTP 437	
Db	301	DNSGTIDYSEFTAAATLHNKMKREBEHLVAAFOYFDKQSGFITIDELQQACVERGMADV 360	
QY	438	LDMIKIEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADA 485	
Db	361	LEDIIEVDQNDGKIDYGEFVEMMQKNAGVGR-RTWRNSLINISMRDA 408	
RESULT 14			
AAG46565			
ID	AAG46565 standard; Protein; 463 AA.		
XX			
AC	AAG46565;		
XX			
DT	18-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 58596.		
XX			
KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	06-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128234.	
PR	16-APR-1999;	99US-0128714.	
PR	13-APR-1999;	99US-0129845.	
PR	21-APR-1999;	99US-0130077.	
PR	23-APR-1999;	99US-0130510.	
PR	23-APR-1999;	99US-0130891.	
PR	28-APR-1999;	99US-0131449.	
PR	30-APR-1999;	99US-0132048.	
PR	30-APR-1999;	99US-0132407.	
PR	04-MAY-1999;	99US-0132484.	
PR	05-MAY-1999;	99US-0132485.	
PR	06-MAY-1999;	99US-0132486.	
PR	06-MAY-1999;	99US-0132487.	
PR	07-MAY-1999;	99US-0132863.	
PR	11-MAY-1999;	99US-0134256.	
PR	14-MAY-1999;	99US-0134218.	
PR	14-MAY-1999;	99US-0134219.	
PR	14-MAY-1999;	99US-0134221.	
PR	14-MAY-1999;	99US-0134370.	
PR	18-MAY-1999;	99US-0134768.	
PR	19-MAY-1999;	99US-0134941.	
PR	20-MAY-1999;	99US-0135124.	
PR	21-MAY-1999;	99US-0135353.	
PR	24-MAY-1999;	99US-0135629.	
PR	25-MAY-1999;	99US-0136021.	
PR	27-MAY-1999;	99US-0136592.	
PR	28-MAY-1999;	99US-0136782.	
PR	01-JUN-1999;	99US-0137222.	
PR	03-JUN-1999;	99US-0137528.	

PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138647.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149268.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149375.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0152070.
PR	29-JUN-1999;	99US-0140391.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0143277.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143824.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0158293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0158294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0158295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159684.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160984.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145313.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145318.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	03-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	04-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	05-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			

Query Match 57.9%; Score 1501; DB 21; Length 463;  
Best Local Similarity 61.4%; Pred. No. 4.4e-135;

Matches 281; Conservative 79; Mismatches 92; Indels 6; Gaps 3;

QY 26 YILGKLGQGGTGYLTCTKSTANVACKSIPKRLVCRDYEVDVREIOIMHLSHP 85  
 DB 8 YSLGKLGQGGTGYLTCTKSTANVACKSIPKRLVCRDYEVDVREIOIMHLSHP 67  
 QY 86 NVVRIGKTYEDSVFVHIVMEVCEGSELDFTVSKGHFSEREAVKLIKTILGVVEACHSLG 145  
 DB 68 NVEIKGAYEDKSHVHIVMEVCEGSELDFTVSKGHFSEREAVKLIKTILGVVEACHSLG 127  
 QY 146 VMHRLKPFNFDSKDDAKLKPATDFGLSVFYKPGQYLDVVGSPYVVAPEVLKCYGP 205  
 DB 128 VTHRLKPFNFDSKDDAKLKPATDFGLSVFYKPGQYLDVVGSPYVVAPEVLKCYGP 187  
 QY 206 EIDVNSAGVILVILSGVPPFAETESGIFRQILQGLDKDPKSDPWTISEAAKDLIVKML 265  
 DB 188 EADISIGVILVILSGVPPFAETESGIFRQILQGLDKDPKSDPWTISEAAKDLIVKML 247  
 QY 266 ERSKPKRISAHEALCHPWIVDEQAAPDPLPAVLRLKQFSQNMKIKKALRVIAERLS 325  
 DB 248 NSDPKQRLTAAGVLAHPKEDGEADPVLDPNAVMSRLKQFKAMNFKVALRVIAERLS 307  
 QY 326 EBEIGLKLKELFMIDTNSGTTTPEELKAGLKVYSGELMESEIKSLMDADIDNSGTIDY 385  
 DB 308 EBEIGLKLKELFMIDTNSGTTTPEELKAGLKVYSGELMESEIKSLMDADIDNSGTIDY 367  
 QY 386 GEFLAATLHMNMEREIEIVAFSDFDKDGGYITIDELQSACTEFGLCD-TPLDMMIKE 444  
 DB 368 GFETATWHINLDRHEELHLYSAFHFDKNSGYITMELEQALREFGNDGRDIKEIIE 427  
 QY 445 IOLDNDGKIDFSEFTAMRKQ--DGVGRSRMTMKULNF 480  
 DB 428 VDGNDGRINYDEFVAMVRKGNPDPIPKR---RELSP 462

RESULT 15  
 ID AAG65758 standard; Protein; 280 AA.  
 AC AAG65758;  
 DT 07-JAN-2002 (first entry)  
 DE ATCDPK2 kinase domain sequence.  
 KW Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK2;  
 OS Arabidopsis thaliana.  
 PN WO200168920-A1.  
 PD 20-SEP-2001.  
 PF 13-MAR-2001; 2001WO-US07999.  
 PR 13-MAR-2000; 2000US-189074P.  
 PA (GENO) GEN HOSPITAL CORP.  
 PI Sheen J;  
 DR WPI; 2001-611395/70.  
 PT Using plant protoplast expression systems for rapidly screening  
 PT libraries of nucleic acids to identify gene that modulate expression of  
 PT target genes -  
 XX Examples; Fig 33; 95pp; English.  
 XX The invention provides a high through-put assay for rapidly screening  
 CC a library of nucleic acid molecules to identify a gene product that  
 CC modulates expression of a gene of interest in plant protoplasts. The

method comprises: (1) introducing into 1 or more plant protoplasts:  
 (a) a reporter gene construct operably linked to a promoter of a gene of  
 interest; and (b) a member of a library of nucleic acid molecules (the  
 library member is expressed in the plant protoplasts); and (2) screening  
 the protoplasts to determine whether the amount of gene expression of the  
 reporter gene construct changes in response to the expression of the  
 library members, a change in gene expression of the reporter gene  
 construct identifying the gene product expressed by the library member as  
 1 that modulates expression of the gene of interest. The present sequence  
 represents the amino acid sequence of Arabidopsis calcium dependant  
 protein kinase (CDPK) ATCDPK2 kinase domain.

Query Match 57.8; Score 1500; DB 22; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-125;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PSNTVLVPTPLRDHYLLGKLGQGGTGYLTCTKSTANVACKSIPKRLVCRDYE 69  
 DB 1 PSNTVLVPTPLRDHYLLGKLGQGGTGYLTCTKSTANVACKSIPKRLVCRDYE 60  
 QY 70 DVREIOIMHLSHPNVVRIGKTYEDSVFVHIVMEVCEGSELDFTVSKGHFSEREAVK 129  
 DB 61 DVREIOIMHLSHPNVVRIGKTYEDSVFVHIVMEVCEGSELDFTVSKGHFSEREAVK 120  
 QY 130 LIKTILGVVEACHSLGVHMRDLKPFNFDSKDDAKLKPATDFGLSVFYKPGQYLDVVG 189  
 DB 121 LIKTILGVVEACHSLGVHMRDLKPFNFDSKDDAKLKPATDFGLSVFYKPGQYLDVVG 180  
 QY 190 SPYVVAPEVLKCYGPEDVMSAGVILVILSGVPPFAETESGIFRQILQGLDKPDKSDP 249  
 DB 181 SPYVVAPEVLKCYGPEDVMSAGVILVILSGVPPFAETESGIFRQILQGLDKPDKSDP 240  
 QY 250 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 289  
 DB 241 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 280

Search completed: February 13, 2003, 21:09:11  
 Job time : 62 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 21:08:08 ; Search time 22 Seconds  
(without alignments)  
662.016 Million cell updates/sec

Title: US-09-848-806-1  
Perfect score: 2593  
Sequence: 1 METKPNRPSTNVLPTQTP.....KMLNFNIADAFVDGKSDS 495

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA.\*
- 1: /cgn2\_6/prodata/2/aa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/prodata/2/aa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/prodata/2/aa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/prodata/2/aa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/prodata/2/aa/PCUTS\_COMB.pep.\*
  - 6: /cgn2\_6/prodata/2/aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1927	74.3	463	1 US-07-951-715A-25	Sequence 25, Appl
2	1927	74.3	463	2 US-08-459-448A-25	Sequence 25, Appl
3	1927	74.3	463	3 US-08-459-595A-25	Sequence 25, Appl
4	1927	74.3	463	3 US-08-459-504B-25	Sequence 25, Appl
5	1927	74.3	463	3 US-08-459-444-25	Sequence 0, Appl
6	1927	74.3	463	4 US-08-547-422-25	Sequence 0, Appl
7	1672.5	64.5	639	4 US-09-347-801-17	Sequence 17, Appl
8	1437.5	55.4	464	1 US-07-951-715A-22	Sequence 22, Appl
9	1437.5	55.4	464	2 US-08-459-448A-22	Sequence 22, Appl
10	1437.5	55.4	464	3 US-08-459-595A-22	Sequence 22, Appl
11	1437.5	55.4	464	3 US-08-459-504B-22	Sequence 22, Appl
12	1437.5	55.4	464	3 US-08-459-444-22	Sequence 0, Appl
13	1437.5	55.4	464	4 US-09-347-422-22	Sequence 0, Appl
14	1277.5	49.3	408	1 US-07-951-715A-21	Sequence 21, Appl
15	1277.5	49.3	408	2 US-08-459-448A-21	Sequence 21, Appl
16	1277.5	49.3	408	3 US-08-459-595A-21	Sequence 21, Appl
17	1277.5	49.3	408	3 US-08-459-504B-21	Sequence 21, Appl
18	1277.5	49.3	408	3 US-08-459-444-21	Sequence 21, Appl
19	1277.5	49.3	408	4 US-09-347-422-21	Sequence 21, Appl
20	829	32.0	623	4 US-08-347-801-4	Sequence 4, Appl
21	826	31.9	625	4 US-09-347-801-18	Sequence 18, Appl
22	800	30.9	576	4 US-09-347-801-19	Sequence 19, Appl
23	771.5	29.8	456	1 US-08-464-164-2	Sequence 2, Appl
24	771.5	29.8	456	1 US-08-338-057-2	Sequence 2, Appl
25	771.5	29.8	456	1 US-08-368-416-2	Sequence 2, Appl
26	622	24.0	520	4 US-09-357-825B-20	Sequence 20, Appl
27	587.5	22.7	370	2 US-08-878-989-19	Sequence 19, Appl

28	587.5	22.7	370	4	US-09-372-796-19	Sequence 19, Appl
29	587.5	22.7	370	4	US-09-457-040B-31	Sequence 31, Appl
30	582	22.4	517	4	US-09-357-825B-21	Sequence 21, Appl
31	548	21.1	264	2	US-07-857-224B-19	Sequence 19, Appl
32	543.5	21.0	556	4	US-09-800-960-4	Sequence 4, Appl
33	539	20.8	565	4	US-09-800-960-2	Sequence 2, Appl
34	538	20.7	264	2	US-07-857-224B-18	Sequence 18, Appl
35	535.5	20.7	424	2	US-08-715-568A-1	Sequence 1, Appl
36	533.5	20.6	387	1	US-08-713-828-3	Sequence 3, Appl
37	533.5	20.6	387	2	US-08-919-627-3	Sequence 3, Appl
38	533.5	20.6	387	2	US-08-096-245-3	Sequence 3, Appl
39	533.5	20.6	387	4	US-09-457-040B-30	Sequence 30, Appl
40	532.5	20.5	343	2	US-08-878-989-5	Sequence 5, Appl
41	532.5	20.5	343	2	US-09-272-796-5	Sequence 5, Appl
42	530	20.4	295	1	US-07-951-715A-23	Sequence 23, Appl
43	530	20.4	295	2	US-08-459-448A-23	Sequence 23, Appl
44	530	20.4	295	3	US-08-459-595A-23	Sequence 23, Appl
45	530	20.4	295	3	US-08-459-504B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-07-951-715A-25  
; Sequence 25, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18905/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..463  
OTHER INFORMATION: /note= "protein sequence for  
OTHER INFORMATION: soybean CDPK as shown in Figure 34."  
US-07-951-715A-25

Query Match 74.3%; Score 1927; DB 1; Length 463;

Best Local Similarity 78.7%; Pred. No. 1e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYOTPLRDLHYLLGKLGQGGFGTTTLCTEKSTSNVACKSIKPKLVCRDVEDYWR 73  
DB 1 VLPQSTQNIREVVEVGRKLGQGGFGTTTCTRAGSGKFAKSIKPKLLCKEDYEDYWR 60  
QY 74 EIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLIKT 133  
DB 61 EIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLIKT 120  
QY 134 ILGVVEACHSLGVNHRDLKPEFLFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
DB 121 IVEVVEACHSLGVNHRDLKPEFLFDTIDEDAKLKATDFGLSVFYKPGESCDVVGSPPY 180  
QY 194 VAPVLLKVCYGEIDVWSAGVILYLLSGVPPFWABTEGIFRQILQKLFDPKDPWPTI 253  
DB 181 VAPEVLRKLYGPESDVWSAGVILYLLSGVPPFWABTEGIFRQILQKLFDPKDPWPTI 240  
QY 254 SEAAKLIYKMLERSPKKRIKSAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSOMNLIK 313  
DB 241 SDSAKDLIRKMLDQNPTRLTATHEVLRHPWVDNTPDKPLDSAVLSRLKQFSAMNLIK 300  
QY 314 KQALRVIAERLSEEEIGGLKELPKMTDNTSGTITPEELKAGLKRVGSELMSEIKSLMD 373  
DB 301 KQALRVIAERLSEEEIGGLKELPKMTDNTSGTITPEELKAGLKRVGSELMSEIKSLMD 360  
QY 374 AADIDNSGTIDYGEFFLAATLHMNMKREELVAAFDKDFKDGSGVITIDELQSACTEFL 433  
DB 361 AADIDKSGTIDYGEFFAATVHLNKLREELVSAFVFKDGSGVITIDELQSACTEFL 420  
QY 434 CDTPLDMKXIDLDNCKIDPSEFTAMRKGD-GVGRSRTWK 476  
DB 421 DDIHDDMIKEIDQDNDGQIDYGEFFAAMRKGNNGGIGR-RTWRK 463

RESULT 2

US-08-459-448A-25  
Sequence 25, Application US/08459448A  
Patent No. 5853336

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 589336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA: US 07/951,715  
APPLICATION NUMBER: 25-SEP-1992  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..463  
OTHER INFORMATION: /note= "protein sequence for  
OTHER INFORMATION: soybean CDPK as shown in Figure 34."  
US-08-459-448A-25

Query Match 74.3%; Score 1927; DB 2; Length 463;

Best Local Similarity 78.7%; Pred. No. 1e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYOTPLRDLHYLLGKLGQGGFGTTTLCTEKSTSNVACKSIKPKLVCRDVEDYWR 73  
DB 1 VLPQSTQNIREVVEVGRKLGQGGFGTTTCTRAGSGKFAKSIKPKLLCKEDYEDYWR 60  
QY 74 EIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLIKT 133  
DB 61 EIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSREAVKLIKT 120  
QY 134 ILGVVEACHSLGVNHRDLKPEFLFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
DB 121 IVEVVEACHSLGVNHRDLKPEFLFDTIDEDAKLKATDFGLSVFYKPGESCDVVGSPPY 180  
QY 194 VAPVLLKVCYGEIDVWSAGVILYLLSGVPPFWABTEGIFRQILQKLFDPKDPWPTI 253  
DB 181 VAPEVLRKLYGPESDVWSAGVILYLLSGVPPFWABTEGIFRQILQKLFDPKDPWPTI 240  
QY 254 SEAAKLIYKMLERSPKKRIKSAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSOMNLIK 313  
DB 241 SDSAKDLIRKMLDQNPTRLTATHEVLRHPWVDNTPDKPLDSAVLSRLKQFSAMNLIK 300  
QY 314 KQALRVIAERLSEEEIGGLKELPKMTDNTSGTITPEELKAGLKRVGSELMSEIKSLMD 373

Db 301 KVALVIAERLSEIEIGGLKELFKMIDTNSGTTTFDELKQGLKRVGSELMSEIKDLMD 360  
QY 374 AADINSGTIDYGEFLAATLHMKNKEREELVAAFSDFDKDGGYITIDELQSACTEFG 433  
Db 361 AADIDKSGTIDYGEFLAATVHLNKLREENLVSAFSDKDGSGYITIDELQOACKDFGL 420  
QY 434 CDTPLDDMIKEIDLNDGKIDPSEPTAMRKGD-GVGRSRTMMK 476  
Db 421 DDIHDDMIKEIDLNDGQIDYGEFAAMVRKNGGIGR-RTMRK 463

RESULT 3  
US-08-459-595A-25  
Sequence 25, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,595A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..463  
OTHER INFORMATION: /note= "protein sequence for  
OTHER INFORMATION: soybean CDPK as shown in Figure 34."  
US-08-459-595A-25  
Query Match 74.3%; Score 1927; DB 3; Length 463;  
Best Local Similarity 78.7%; Pred. No. 1e-152;  
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;  
QY 14 VLPYQTPRLRDHYLLGKLGOGFGTTLCTEKSTANVACKSIPKRLKLVCRDYEYDVR 73  
Db 1 VLPQRTQNVREVVEVGRKLGOGFGTTFCTRRASGGKPAKSIIPKRLCKEDYEDVR 60  
QY 74 EIQIMHLSHPNVVRIKGTYESVFIHVMVECEGELFDRIVSKGHFSEREAVKLIKT 133  
Db 61 EIQIMHLSHPNVVRIEGTVEDSTAVHLMELCEGELFDRIVQKGYSEQAARLIKT 120  
QY 134 ILGVVEACHSLGVNHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLYDVGSPYY 193  
Db 121 IVEVVEACHSLGVNHRDLKPNFLFDDAKLKATDFGLSVFYKPGSFCDVVGSPYY 180  
QY 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILQGLDKFSDPMTI 253  
Db 181 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILQGLDKFSDPMTI 240  
QY 254 SEAAKDLIYKMLERSPKRISAHEALCHPWIVDEQAAPDKPLPAVLRLKQFSQNNKIK 313  
Db 241 SDSAKDLIRKMLDQNPXTRLTAEVLRHPWIVDNDIAPDKPLDSAVLSRLKQFSAMNKLK 300  
QY 314 KVALVIAERLSEIEIGGLKELFKMIDTNSGTTTFDELKQGLKRVGSELMSEIKSLMD 373  
Db 301 KVALVIAERLSEIEIGGLKELFKMIDTNSGTTTFDELKQGLKRVGSELMSEIKDLMD 360  
QY 374 AADINSGTIDYGEFLAATLHMKNKEREELVAAFSDFDKDGGYITIDELQSACTEFG 433  
Db 361 AADIDKSGTIDYGEFLAATVHLNKLREENLVSAFSDKDGSGYITIDELQOACKDFGL 420  
QY 434 CDTPLDDMIKEIDLNDGKIDPSEPTAMRKGD-GVGRSRTMMK 476  
Db 421 DDIHDDMIKEIDLNDGQIDYGEFAAMVRKNGGIGR-RTMRK 463

RESULT 4  
US-08-459-504B-25  
Sequence 25, Application US/08459504B  
Patent No. 6075185  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 6075185artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park

```

QY 434 CDTPLDDMIKIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
DB 421 DDHIDDMIKIDQNDQGDIDYGEFAAMRRKGGIGR-RTMRK 463

RESULT 5
US-08-459-444-25
; Sequence 0, Application US/08459444
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/PL/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 74.3%; Score 1927; DB 3; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYOTPLRHHLLGKLGQGGTGYTLCTEKSTANYACKSIPKELVCREDYEDVNR 73
DB 1 VLPQTONIREVYEVGRKLGQGGTTFECTRRASGGKFAKCSIPKELCKEDYEDVNR 60
QY 74 EIQIMHLSSEHNVRIGTYEDSVFVHIVMEVCEGGELTDRIVSKGHFSEBAVKLIKT 133
DB 61 EIQIMHLSSEHANVRIEGTYEDSTAVELVMECEGGELFDRIYVQKHYSERQAARLIKT 120
QY 134 ILGVVEACHSLGVHARDLKPENFLFDSKDKAKATDFGLSVFYKPGQYLYDVVGSPPY 193
DB 121 IVEVVEACHSLGVHARDLKPENFLFDTIDEAKAKATDFGLSVFYKPGSEFCDVVGSPPY 180
QY 194 VAPEVLKCYGPEIDVWAGVILYLLSGVPPFAETSGIFRQILQKLDLDFKSDPPTI 253
DB 181 VAPEVLRLKLYGPESDVWAGVILYLLSGVPPFAESEPFIQRIILLGLKLDLDFHSEWPFI 240
QY 254 SEAAKDLIYKMLERSPKKRISEALCHPWTVDQAPDKPLDPAVLRLKQFSQMNKIK 313
DB 241 SUSAKDLIRKMLDQPKRLTAHEVRLPWIVDDNIAEPKLDGSAVLRLKQFSAMNKLK 300
QY 314 KVALRVIAERLSEEEIGGLKEIKFMIDTNSGTTTFEELKAGLKRVSSELMESIKLMD 373
DB 301 KVALRVIAERLSEEEIGGLKEIKFMIDTNSGTTTFEELKAGLKRVSSELMESIKLMD 360
QY 374 AADIDNSGTDYGEFIAATLHMKNKVEREILVAAPSDFKDQSGVITIDELQSACTEFG 433
DB 361 AADIDKSGTDYGEFIAATVHLNKUREENLVSAFSPDKQSGVITIDELQSACTEFG 420

```

Db 1 VLPQRTQNTREVVEVGRKLGQGFQGTTFCTRRASGGKFAKSPKRLKLLCKEDYEDVWR 60  
QY 74 EIQIMHLSLSEHPNVRIKTYEDSVFVHVMVEVCGGELFDRIVSKGHFSREAVKIKT 133  
Db 61 EIQIMHLSLSEHANVRIEGTYEDSTAVHLVLMELCGGELFDRIVQKGYHSEQAARLIKT 120  
QY 134 ILGVWACHSLGVMHRLKPEFLPDSKDDAKLKAATDGLSVFYKPGCYLYDVVVGSPYY 193  
Db 121 IVEVWACHSLGVMHRLKPEFLPFTTIDEDAKLKAATDGLSVFYKPGSECDVVVGSPYY 180  
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKFDKSDPWPPTI 253  
Db 181 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKFDHSEPPWPSI 240  
QY 254 SEAKOLIVKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNLIK 313  
Db 241 SDSAKOLIRKMLDQNPKEKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLRLKQFSAMNLIK 300  
QY 314 KVALRVIARLSLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKVGSSELMESEIKSLMD 373  
Db 301 KVALRVIARLSLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKVGSSELMESEIKSLMD 360  
QY 374 AADIDNSGTIDYGEFIAATVHLNKLRENLVSAFSDYFDKGGSGYITIDELQSACTEFL 433  
Db 361 AADIDNSGTIDYGEFIAATVHLNKLRENLVSAFSDYFDKGGSGYITIDELQSACTEFL 420  
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476  
Db 421 DDIHIDMIKEIDQNDGQIDYGEFAAMRKNGGIGR-RTMRK 463

RESULT 6  
US-09-547-422-25  
; Sequence 0, Application US/09547422  
; Patent No. 6320100  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.  
; Warren, Gregory W.  
; Evola, Stephen V.  
; Crossland, Lyle D.  
; Wright, Martha S.  
; Merlin, Ellis J.  
; Lounis, Karen L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/547,422  
; FILING DATE: 11-Apr-2000  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/459,595  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:

; NAME: Weigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-18805H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for  
; soybean CDPK as shown in Figure 34."  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 463 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..463  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-547-422-25  
  
Query Match 74.3%; Score 1927; DB 4; Length 463;  
Best Local Similarity 78.7%; Pred. No. 1e-152;  
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;  
  
QY 14 VLPYQTPRLRDHYLLGKLGQGFQGTTFCTRRASGGKFAKSPKRLKLLCKEDYEDVWR 73  
Db 1 VLPQRTQNTREVVEVGRKLGQGFQGTTFCTRRASGGKFAKSPKRLKLLCKEDYEDVWR 60  
QY 74 EIQIMHLSLSEHPNVRIKTYEDSVFVHVMVEVCGGELFDRIVSKGHFSREAVKIKT 133  
Db 61 EIQIMHLSLSEHANVRIEGTYEDSTAVHLVLMELCGGELFDRIVQKGYHSEQAARLIKT 120  
QY 134 ILGVWACHSLGVMHRLKPEFLPDSKDDAKLKAATDGLSVFYKPGCYLYDVVVGSPYY 193  
Db 121 IVEVWACHSLGVMHRLKPEFLPFTTIDEDAKLKAATDGLSVFYKPGSECDVVVGSPYY 180  
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKFDKSDPWPPTI 253  
Db 181 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIFRQILQKLDKFDHSEPPWPSI 240  
QY 254 SEAKOLIVKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNLIK 313  
Db 241 SDSAKOLIRKMLDQNPKEKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLRLKQFSAMNLIK 300  
QY 314 KVALRVIARLSLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKVGSSELMESEIKSLMD 373  
Db 301 KVALRVIARLSLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKVGSSELMESEIKSLMD 360  
QY 374 AADIDNSGTIDYGEFIAATVHLNKLRENLVSAFSDYFDKGGSGYITIDELQSACTEFL 433  
Db 361 AADIDNSGTIDYGEFIAATVHLNKLRENLVSAFSDYFDKGGSGYITIDELQSACTEFL 420  
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476  
Db 421 DDIHIDMIKEIDQNDGQIDYGEFAAMRKNGGIGR-RTMRK 463

RESULT 7  
US-09-347-801-17  
; Sequence 17, Application US/09347801  
; Patent No. 6262345  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/347,801  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: 60/092,438  
; EARLIER FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97

```

; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-17

Query Match          64.5%; Score 1672.5; DB 4; Length 639;
Best Local Similarity 66.2%; Pred. No. 2.6e-131;
Matches 318; Conservative 66; Mismatches 93; Indels 13; Gaps 3;

QY 5 PNPR-RPS-----NTVLPYQTPRLRDHYLLGKKGQGFYTYLCTEKTSANY 52
Db 120 PSRPRPQVKRVSSAGLLGSLVLRKKTENLKDYSIGRLGQGFYTHLCVERATGKEL 179

QY 53 AKSIPKRLVCREDEVDWRRIQIWMHLSHPNVRKGTIYEDSVFVHVMVCEGGEL 112
Db 180 ACSILKRLGSDDDVEDVRRIQIMHLAGHPSVVGIRGAYEDAVAVHVMVCEGGEL 239

QY 113 FDRIVSKGHFSREAVKLIKTLGVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDF 172
Db 240 FDRIVRGHYTERKAAELARVIVGVVEACHSGMGNHRDLKPENFLFADHSEEAALKTIDF 299

QY 173 GLSVFYKPGQYLDVVGVSPYVAPVLAKEKCPEDVWSAGVILYLLSGVPPFMAETES 232
Db 300 GLSIFPRPGQITDVGSPYVAPVLAKEKCPEDVWSAGVILYLLSGVPPFMAETES 359

QY 233 GIPRQIQLGKLFKPSDMPWTISEAAKDIYKMLERSPKRISAEALCHPMIVDEQAAPD 292
Db 360 GIPFVHLGRDLFSESEPPSISDGAADLVRRMLVRDPRKRLTAHEVLRHPWQVGVGAPD 419

QY 293 KPLDPAVLRLKQFSOMNKIKOMARVIAERLSSEEGGLKELFMKTDITNSGTITFEEL 352
Db 420 RPLDSAVLSRMKQFSAMNKLKOMARVIAERLSSEEGGLKELFMKTDITNSGTITFEEL 479

QY 353 KAGLRVSGELMESIKSLMDADINDSGTIDYGEFFAATLHMNMKREILVAATSDFD 412
Db 480 KVGLEKVGANLQESSIYALMQAADVNNGTIDYGEFFAATLHMNMKREILVAATSDFD 539

QY 413 KOGSGYITIDELQSACTEGLCDTFLDDMKIEIDLNDGKIDFSEFTAMVRKGVGRSR 472
Db 540 KOGSGYITADELQVACEBGLGDVQLELDLGEVDODNDGRIDYNEFVAMNQK-PTVGGSR 598

RESULT 8
US-07-951-715A-22
; Sequence 22, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Ralini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Leunis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA

```

```

ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30B
CURRENT APPLICATION DATA: US/07/951.715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 04-OCT-1991
APPLICATION NUMBER: US 07/772,027
ATTORNEY/AGENT INFORMATION:
NAME: Strull, M. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELEPHONE: (919) 541-8615
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
US-07-951-715A-22
Query Match          55.4%; Score 1437.5; DB 1; Length 464;
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRDEHYLLGKKGQGFYTYLCTEKTSANYACKSIKRLVCREDEVDWRRIQIMHHL 81
Db 9 VRATYSGKELGQGFYTHLCVTHRTSGEKLACTIAKRLAAREDDVDRVREVDVQINHL 69

QY 82 SEHPNVVRKGTIYEDSVFVHVMVCEGGELFDRIVSKGHFSREAVKLIKTLGVVEAC 141
Db 69 SQGPVVGLRGAYEDKQSVHLMELCAGGELFDRIVARGQYTERGAELRAIVQIVHTC 128

QY 142 HSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQYLDVVGVSPYVAPVLAKE 202
Db 129 HSMGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQYLDVVGVSPYVAPVLAKE 188

QY 202 CYGPEIDVMSAGVILYLLSGVPPFMAETESGIFRQLQGLKDFKSDPWTISEAAKDLI 261
Db 189 KYGPEADIVMSAGVILYLLSGVPPFMAETESGIFRQLQGLKDFKSDPWTISEAAKDLI 248

QY 262 YKMLERSPKRISAEALCHPMIVDEQAAPKPLDPAVLSELKQFSOMNKIKOMARVIA 321
Db 249 KMLNINPRERLTAFOVLAHPMKEDGAPDTPLDNNVLDRLKQFRANQPKKALRIIA 308

QY 322 ERLSEEEIGGLKELFMKTDITNSGTITFEELKAGLRVSGELMESIKSLMDADINDSG 381
Db 309 GCLSEEEITGLKEMFNKIDKNSGTITLDELKGLAKHGPXKLSDEMEKLEAADAAGNG 368

QY 382 TIDYGEFFAATLHMNMKREILVAATSDFPKDGSGYITIDELQSACTEGLCDT-PLDD 440
Db 369 LIIDYGEFFAATLHMNMKREILVAATSDFPKDGSGYITIDELQSACTEGLCDT-PLDD 428

QY 441 MIKEIDLNDGKIDFSEFTAMVRKGV 465
Db 429 IISDADSDNDGRIDYNEFVAMVRKGV 453

RESULT 9

```



```

1 APPLICANT: Kramer, Vance C.
2 APPLICANT: Warren, Gregory W.
3 APPLICANT: Evola, Stephen V.
4 APPLICANT: Crossland, Lyle D.
5 APPLICANT: Wright, Martha S.
6 APPLICANT: Merlin, Ellis J.
7 APPLICANT: Launis, Karen L.
8 APPLICANT: Rothstein, Steven J.
9 APPLICANT: Bowman, Cindy G.
10 APPLICANT: Dawson, John L.
11 APPLICANT: Dunder, Erik M.
12 APPLICANT: Pace, Gary M.
13 APPLICANT: Suttie, Janet L.
14 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
15 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
16 NUMBER OF SEQUENCES: 94
17 CORRESPONDENCE ADDRESS:
18 ADDRESSEE: No. 607518artis Corporation
19 STREET: 3054 Cornwallis Road
20 CITY: Research Triangle Park
21 STATE: NC
22 COUNTRY: USA
23 ZIP: 27709
24 COMPUTER READABLE FORM:
25 MEDIUM TYPE: Floppy disk
26 COMPUTER: IBM PC compatible
27 OPERATING SYSTEM: PC-DOS/MS-DOS
28 SOFTWARE: Patent In Release #1.0, Version #1.30
29 CURRENT APPLICATION DATA:
30 APPLICATION NUMBER: US/08/459,504B
31 FILING DATE:
32 CLASSIFICATION:
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 08/459,595
35 FILING DATE: 02-JUN-1995
36 APPLICATION NUMBER: US 07/951,715
37 FILING DATE: 25-SEP-1992
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 07/772,027
40 FILING DATE: 04-OCT-1991
41 ATTORNEY/AGENT INFORMATION:
42 NAME: Meigs, J. Timothy
43 REGISTRATION NUMBER: 38,241
44 REFERENCE/DOCKET NUMBER: CSCI577/CIP/DIV
45 TELECOMMUNICATION INFORMATION:
46 TELEPHONE: (919)541-8587
47 TELEFAX: (919)541-8689
48 INFORMATION FOR SEQ ID NO: 22:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 464 amino acids
51 TYPE: amino acid
52 STRANDEDNESS: single
53 TOPOLOGY: linear
54 MOLECULE TYPE: protein
55 HYPOTHETICAL: NO
56 FEATURE:
57 NAME/KEY: Protein
58 LOCATION: 1..464
59 OTHER INFORMATION: /note= "derived protein sequence of
60 OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
61 US-08-459-504B-22
62
63 Query Match 55.4%; Score 1437.5; DB 3; Length 464;
64 Best Local Similarity 60.9%; Pred. No. 6,7e-112;
65 Matches 274; Conservative 70; Mismatches 103; Indels 1; Gaps
66
67 QY 22 LRDHVLLGKGLGQGGTGYLTCTEXTSANTYACKSIKPKLVCRDEYDVWREIQIMHHL 81
68 9 VRATYSNGKELGRGQGVTHLCTHRTSGEKLAACKTAKRKLAAERDVEDVDREVQIMHHL 68
69
70 QY 82 SEHNPNVRIKGTVEDSVFHVIMVEVCEGELFDRIVSKGHFSREAVKLIKILGWVAC 141
71 DB 69 SQGNPNVGLRGVAYEQSVHLYMVELCAGELFDRILFARGGYTERGAELRLAIVQIVHTC 128

```

142 HSLGVMHDLKXENFLDPSKODAKLKTDFGLSVFYKPGQYLDVVGSPYYVAPEVLKK 201  
129 HSMGVNHRDIKPEFLLSKDEDAPLKATDFGLSVFYKPGQYLDVVGSPYYVAPEVLKK 188  
202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDFKSDPWPPTISEAAKDLI 261  
199 KYGPEADWSVGVMYIFLAGVPPFWAENENGIFTAILRQGLDLSSEPPWPHISPGAKDLV 248  
262 YKMLERSPKKISAEALCHWIVDEQAAPDKPLDPVLSRLKQFOSQNNKIKKMAALRVIA 321  
249 KMLNINPKERLTAFQVNLNHWIKEDGAPDTPDNLNVLRLKQFRANQFKKAALRIIA 308  
322 ERLSBEETGLKELFKMIDTNSGTTITPEELKAGLKRVSSELMSEIKSLMDAADIDNSG 381  
309 GCLSEETGLKEMFNKIDKNSGTTITLDELKHGLAKHPKLSDEMEKLEAADAADGNG 368  
382 TIDYGEFLAALHWNKMERELVNAFSDPKDGSYITIDELQSACTEGLCDT-PLDD 440  
369 LIDYDEFVTATVHNNKLDREHLYTAFQYFDKNSGYITKEELEHALKEOGLYDADKIKD 428  
441 MIKEIDLNDGKIDSEFTAMMRKG 465  
429 IISDADSDNGRIDYSEFVAMMRKG 453

RESULT 12  
US-08-459-444-22  
; Sequence 0, Application US/08459444A  
; Patent No. 6121014  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauis, Karen L.  
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED  
NUCLEIC ACID CODING SEQUENCE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of

pollen specific CDPK as disclosed in Figure 34."  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..464  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-08-459-444-22  
Query Match 55.4%; Score 1437.5; DB 3; Length 464;  
Best Local Similarity 60.9%; Pred. No. 6.7e-112;  
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;  
QY 22 LRHYVLLGKLGQGFQGTLYLCTEKSTANYACKSIPKRLVCREDYEDVWREIQIMHHL 81  
Db 9 VRATYSVKEGLGRQFGVTHLCHTRTSGEKLACKTAKKLAAREDDVDVREVQIMHHL 68  
QY 82 SEHPNVVRIKGTYESVFMVMEVCEGGELFDRIVSKGHFSEREAVKLIKILGVVEAC 141  
Db 69 SQQENVVGLRGAYEDKQSVHLVWELCAGGELFDRITARGQYTERGAELLRAIVQIVHTC 128  
QY 142 HSLGVMHDLKXENFLDPSKODAKLKTDFGLSVFYKPGQYLDVVGSPYYVAPEVLKK 201  
Db 129 HSMGVNHRDIKPEFLLSKDEDAPLKATDFGLSVFYKPGQYLDVVGSPYYVAPEVLKK 188  
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDFKSDPWPPTISEAAKDLI 261  
Db 189 KYGPEADWSVGVMYIFLAGVPPFWAENENGIFTAILRQGLDLSSEPPWPHISPGAKDLV 248  
QY 262 YKMLERSPKKISAEALCHWIVDEQAAPDKPLDPVLSRLKQFOSQNNKIKKMAALRVIA 321  
Db 249 KMLNINPKERLTAFQVNLNHWIKEDGAPDTPDNLNVLRLKQFRANQFKKAALRIIA 308  
QY 322 ERLSBEETGLKELFKMIDTNSGTTITPEELKAGLKRVSSELMSEIKSLMDAADIDNSG 381  
Db 309 GCLSEETGLKEMFNKIDKNSGTTITLDELKHGLAKHPKLSDEMEKLEAADAADGNG 368  
QY 382 TIDYGEFLAALHWNKMERELVNAFSDPKDGSYITIDELQSACTEGLCDT-PLDD 440  
Db 369 LIDYDEFVTATVHNNKLDREHLYTAFQYFDKNSGYITKEELEHALKEOGLYDADKIKD 428  
QY 441 MIKEIDLNDGKIDSEFTAMMRKG 465  
Db 429 IISDADSDNGRIDYSEFVAMMRKG 453

RESULT 13  
US-09-547-422-22  
; Sequence 0, Application US/09547422  
; Patent No. 6320100  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park

STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/547,422  
FILING DATE: 11-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8537  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: /notes "derived protein sequence of pollen specific CdpK as disclosed in Figure 34."  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..464  
SEQUENCE DESCRIPTION: SEQ ID NO: 22;  
US-09-547-422-22  
Query Match 55.4%; Score 1437.5; DB 4; Length 464;  
Best Local Similarity 60.9%; Pred. No. 6.7e-112;  
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;  
QY 22 LRHYLLGKLGQGGFTYCTEKSSTANYACKSIPKRLKVCREDYEDVWRDIQMHL 81  
DB 9 VRATYSMGKELGRGQFGVTHLCTHRTSGEKLACTIAKRKLAAEDVDYRREVQIMHL 68  
QY 82 SEHPNVRIKGTYESVVFHVMVEVCGELFDRIVSKGHFSEREAVKLTKTLGVVEAC 141  
DB 69 SQQPNVGLRGAYEDKQSVHLVWELCAGGELFDRIIARGQYTERGAELRAIVQVHC 128  
QY 142 HSLGVNHRDLKPENFLFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGVSPYYVAPEVLKX 201  
DB 129 HSMGVNHRDIKPENFLLSKDEDAFLKATDFGLSVFFKEGELLRDIVGSAYIYIAPEVLK 188  
QY 202 CYGPIDWSAGVILYLLSGVPPWAETESGIFRILGKLFKSDPWPITSEAKDLI 261  
DB 189 KYGPEADWSVGMVLIYIFLAGVPPWAENENGIFAILRGOLDLSSEFPWHISPGAKDLV 248  
QY 262 YKMLERSPKKRIASAEALCHPWIVDEQAAPKPLDPAVLRLKQFQSMNKIKKQALRVIA 321  
DB 249 KQVLNINPKERLTAFQVNLNHPWIKEDGAPDFLDNVLRLKQFRANQPKAALRIIA 308  
QY 322 ERLSEIEGGLKELFMIDTNGSITTEELKAGLRKRVGSELMSEIKSLMDAADIDNSG 381  
DB 309 GCLSEIEITGLKEMFNIDKNSGITITDELKHLAKHPKLSDSMEKLMLEAADADNG 368  
QY 382 TIDYGEFLAATLHMNKEEELIVAAFSDFDKDGSYITIDELASACTEFLGCDT-PLDD 440  
DB 369 LIDYDEVTATVMNKLDRHEHLHTAFQYDFDKDNGSYITKEELEHALKEOGLYDADIKD 428

QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465  
DB 429 IISDADSDNDGRIDYSEFVAMMRKG 453  
RESULT 14  
US-07-951-715A-21  
Sequence 21, Application US/07951715A  
Patent No. 5625136  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Naini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/951,715A  
FILING DATE: 25-SEP-1992  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8615  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 408 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-951-715A-21  
Query Match 49.3%; Score 1277.5; DB 1; Length 408;  
Best Local Similarity 61.9%; Pred. No. 1.2e-98;  
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;  
QY 76 QIMHLSHPNVRIKGTYESVVFHVMVEVCGELFDRIVSKGHFSEREAVKLTKIL 135  
DB 1 QIMHLSGQPNVGLRGAYEDKQSVHLVWELCAGGELFDRIIARGQYTERGAELRAIV 60  
QY 136 GVVEACHSLGVNHRDLKPENFLFSPKDDAKLKATDFGLSVFYKPGQYLYDVVGVSPYYVA 195

Db 61 QIVHTCHSMGVNHRDIKPNFILLSKDEDAFLKATDFGLSVFFKEGELLRDIVGSAYVIA 120  
QY 196 PEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILOGKLDKSPDPWPTISE 255  
Db 121 PEVLKRYGPEADIVSGVGLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEFPWPHISP 180  
QY 256 AAKDLTYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYLSRLKQFQSMNKIKKM 315  
Db 181 GAKDLVKVNLNINPKERLTAFQVLNHPWKEDGDADPTPLDNVLDRLKQFRAMNQPKKA 240  
QY 316 ALRVIAERLSEEEIGGLKELFKQIHTDNGSGITTFEELKAGLKRVGSELMSEIKSLNDAA 375  
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTTLDLKHGLAKHGPKLSDSEMEKLMEEA 300  
QY 376 DIDNSGTIDYGEFLAATLHMKNKVEREILVAAFSDFDXGSGYITIDELQSACTEFGLCD 435  
Db 301 DADGNGLIDYDEFVATVHMNKLDRREHLVTAFOYFDKNSGYITKEELHAKKEQGLYD 360  
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465  
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

RESULT 15

US-08-459-448A-21  
Sequence 21, Application US/08459448A  
Patent No. 5859336  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothschein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dundez, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-5689  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 408 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-448A-21  
Query Match 49.3%; Score 1277.5; DB 2; Length 408;  
Best Local Similarity 61.9%; Pred. No. 1,2e-98;  
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;  
QY 76 QIMHLSHPNVVRIKGTYESVFIHVMVEGEGELFDRIVSKGHFSEREAVKLIKIL 135  
Db 1 QIMHLSGQPNVVGRLGAYEDKQSVHLVLMELCAGGELFDRIIARGQYTERGAAELLRAIV 60  
QY 136 GVVEACHSLGVNHRDLKPELFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVA 195  
Db 61 QIVHTCHSMGVNHRDIKPNFILLSKDEDAFLKATDFGLSVFFKEGELLRDIVGSAYVIA 120  
QY 196 PEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFQILOGKLDKSPDPWPTISE 255  
Db 121 PEVLKRYGPEADIVSGVGLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEFPWPHISP 180  
QY 256 AAKDLTYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAYLSRLKQFQSMNKIKKM 315  
Db 181 GAKDLVKVNLNINPKERLTAFQVLNHPWKEDGDADPTPLDNVLDRLKQFRAMNQPKKA 240  
QY 316 ALRVIAERLSEEEIGGLKELFKQIHTDNGSGITTFEELKAGLKRVGSELMSEIKSLMDAA 375  
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTTLDLKHGLAKHGPKLSDSEMEKLMEEA 300  
QY 376 DIDNSGTIDYGEFLAATLHMKNKVEREILVAAFSDFDXGSGYITIDELQSACTEFGLCD 435  
Db 301 DADGNGLIDYDEFVATVHMNKLDRREHLVTAFOYFDKNSGYITKEELHAKKEQGLYD 360  
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465  
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

Search completed: February 13, 2003, 21:12:42  
Job time : 23 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 21:11:33 ; Search time 19 Seconds

(without alignments)  
665.615 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPENTVLPYQTP.....KNLNFNIADAFVGDGKSD 495

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pap.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pap.\*
- 7: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pap.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pap.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US05\_NEW\_PUB.pap.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US05\_PUBCOMB.pap.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US10\_PUBCOMB.pap.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pap.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1672.5	64.5	639	10	US-09-854-731-17
2	1509.5	58.2	549	10	US-09-828-313-39
3	849	32.7	597	10	US-09-828-313-38
4	828	32.0	623	10	US-09-854-731-4
5	826	31.9	625	10	US-09-854-731-18
6	800	30.9	576	10	US-09-854-731-19
7	587.5	22.7	317	9	US-09-935-464-36
8	587.5	22.7	370	10	US-09-817-181-4
9	554	21.4	357	9	US-10-024-036B-2
10	543.5	21.0	556	12	US-10-096-960-4
11	543	20.9	460	9	US-09-935-464-3
12	543	20.9	476	9	US-09-935-464-5
13	539	20.8	565	12	US-10-096-960-2
14	538.5	20.8	326	10	US-09-817-181-2
15	533.5	20.6	387	10	US-09-771-161A-188
16	510.5	19.7	648	9	US-10-024-036B-5
17	510.5	19.7	817	10	US-09-992-481-4
18	501	19.3	765	9	US-10-217-357-4
19	501	19.3	765	10	US-09-975-326-4

20	501	19.3	766	9	US-09-934-406-2	Sequence 2, Appli
21	501	19.3	766	9	US-10-217-357-2	Sequence 2, Appli
22	501	19.3	766	10	US-09-975-326-2	Sequence 2, Appli
23	496	19.1	385	9	US-10-116-332-2	Sequence 2, Appli
24	489.5	18.9	454	10	US-09-771-161A-238	Sequence 238, App
25	473	18.2	543	10	US-09-740-627-1	Sequence 1, Appli
26	468.5	18.1	280	10	US-09-835-788A-16	Sequence 16, Appli
27	461.5	17.8	405	10	US-09-771-161A-210	Sequence 210, App
28	460	17.7	261	10	US-09-925-299-983	Sequence 983, App
29	457.5	17.6	740	10	US-09-771-161A-265	Sequence 265, App
30	457.5	17.6	740	10	US-09-771-161A-266	Sequence 266, App
31	453	17.5	522	10	US-09-740-627-11	Sequence 11, Appli
32	447.5	17.3	501	10	US-09-797-039-2	Sequence 2, Appli
33	447.5	17.3	501	12	US-10-153-921-2	Sequence 2, Appli
34	446	17.2	1518	10	US-09-801-368-152	Sequence 152, App
35	445.5	17.2	1203	10	US-09-799-875-5	Sequence 5, Appli
36	443	17.1	514	10	US-09-922-138-5	Sequence 2, Appli
37	443	17.1	514	10	US-09-841-683-2	Sequence 2, Appli
38	437	16.9	465	9	US-10-174-784-2	Sequence 2, Appli
39	435	16.8	661	10	US-09-780-949-2	Sequence 2, Appli
40	435	16.8	661	10	US-09-780-949-6	Sequence 6, Appli
41	433	16.7	388	10	US-09-940-921B-7	Sequence 7, Appli
42	431.5	16.6	424	10	US-09-771-161A-257	Sequence 257, App
43	431.5	16.6	424	10	US-09-771-161A-258	Sequence 258, App
44	431.5	16.6	424	10	US-09-771-161A-259	Sequence 259, App
45	431	16.6	398	10	US-09-940-921B-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-854-731-17  
; Sequence 17, Application US/09854731  
; Patent No. US20020120949A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 17  
; LENGTH: 639  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-854-731-17

Query Match	64.5%	Score 1672.5	DB 10	Length 639
Best Local Similarity	66.2%	Pred No. 1.6e-110		
Matches 318	Conservative 66	Mismatches 83	Indels 13	Gaps 3
Qy	5	PNPR-RPS-----NTVLPYQTPRLRHYLLGKLGQGGFGTTLCTEKSTSNY	52	
Db	120	PSPRPQVKRVSSAGLLGSLVLRKNTENLKDYSIGRLGQGGFGTTLCTEKSTSNY	179	
Qy	53	ACSKIPKLVCRDVEDVREIQIMHLSSEHPNVVRIKGTVEDSVFVHVMVCEGGL	112	
Db	180	ACKSILKRLGSDDDVEDVREIQIMHLSSEHPNVVRIKGTVEDSVFVHVMVCEGGL	239	
Qy	113	FDRTVSGHFSEREAVKLINTILGVVVEACHSLGMVHRDLKPNFLFDSFKDAKATDF	172	
Db	240	FDRTVSGHFSEREAVKLINTILGVVVEACHSLGMVHRDLKPNFLFDSFKDAKATDF	299	
Qy	173	GLSVFYKPGQVLDVNGSPYYVAPVLYKCYGPEIDVNSAGVILYLLSGVPPFAETES	232	
Db	300	GLSVFYKPGQVLDVNGSPYYVAPVLYKCYGPEIDVNSAGVILYLLSGVPPFAETES	359	
Qy	233	GIFPQILQGLDKFSPWPPTISEAAKDLIVKMLSPKPKRISAHEALCHPWIVDEQAAPD	292	

Db 360 GIFEVLRGLDFESEPWPSSDGAQLVRMLVRDPKRLTAHEVLRHPWQVGVGAPD 419  
Qy 293 KPLDPAVLSRLKQFSOMNKKKVALRVIAERLSEEEIGGLKELFKMTDNTSNTITFEEL 352  
Db 420 RPLDSAVLSRMKQFANVKKKVALRVIAENLSDEDTAGLREMFMDADNSQITFEEL 479  
Qy 353 KAGLRKVGSELMSEIKSLMDAADINDSGTIDYGEFFLAATLHMNMREBILVAAPSDPD 412  
Db 480 KVGLEKVGANLQSEIYALMQAADVNNGTIDYGEFFLAATLHNMKVEREDHLFAAFQYFD 539  
Qy 413 KDGSYITIDELQSACTEFLGCDTPLDMDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGR 472  
Db 540 KDGSYITADELQVACEEFLGCDVLEDLISEVDNDGRIDYNEFVAMQK-FTVGSR 598

RESULT 2  
US-09-828-313-39  
; Sequence 39, Application US/09828313  
; Patent No. US20020059662A1  
; GENERAL INFORMATION:  
; APPLICANT: COSTA e SILVA, OSWALDO DA  
; APPLICANT: BOHNERT, HANS J.  
; APPLICANT: THIELEN, NOCHA VAN  
; APPLICANT: CHEN, ROUYING  
; APPLICANT: SARRIA-MILLAN, RODRIGO  
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
; FILE REFERENCE: 16313-0032  
; CURRENT APPLICATION NUMBER: US/09/828,313  
; PRIOR APPLICATION NUMBER: 60/196,001  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Physcomitrella patens  
US-09-828-313-39

Query Match 58.2%; Score 1509.5; DB 10; Length 549;  
Best Local Similarity 60.8%; Pred. No. 4,1e-99;  
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;  
Qy 5 PNPRPESNT---VLPQTPRLRDHVLKGLGQGGFTYLTCTEKSANSVACKSPKPK 61  
Db 69 PRKPASRSVGVLCPLSDIQSVILRELGRGQGVYLTCTKNTNEAYACKSAKK 128  
Qy 62 LVCREDYEDVWREIQMHLSHPNVRAIKGTYESDVFIHMEVCEGGLFDRIVSKGH 121  
Db 129 LTSKEDIEDYKREVQIMHLSGTPNIVLVKDFEDKHSVHLVWMLCAGGELFDRIIAKGH 188  
Qy 122 FSREAVKLIKTLGVVEACHSLGVWHRDLKPNFLPDSPKDDAKLKATDFGLSVFKPG 181  
Db 189 YSREAAADCRVIVNVVHRSCHSLGVFHRDLKPNFLASKAEDAPLKATDFGLSTFKPG 248  
Qy 182 QYLYDVVGSYVYVAPVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQLQ 241  
Db 249 DVFQDVGSAVYVAPVLKXSYGPEADVMSAGVIVYLLCGVPPFWAETEQGIFDAVLKG 308  
Qy 242 KLDKSDPMTTISEAAKDLIYKMLERSPKKRISEAHEALCHPWIIVDEQAAPDKPLDP 301  
Db 309 HIDEFENDPFEKTSNGAKDLVRKMLPNVVKIRLTAQVNLNHPMKEDGCPDPLDRAVLT 368  
Qy 302 RLKQFSOMNKKKVALRVIAERLSEEEIGGLKELFKMTDNTSNTITFEELKAGLRKVG 361  
Db 369 RLKNFSAANKMKKALKVIAESLSSEEEIYGLREMPKSDTNTSNTITFEELKEGLLQGS 428  
Qy 362 ELMESEIKSLMDAADINDSGTIDYGEFFLAATLHMNMREBILVAAPSDPDKDGSGYITI 421  
Db 429 KLNESDIRKLMEADVDGNGKIDFNEFISATMHNKTEKEDHLWAAFPNHFDTNSGYITI 488

Qy 422 DELQSACTEFLGCD-TPLDMDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476  
Db 489 DELQSAEAMKNGMGDPETIQEIISEVTDNDGRIDYDFVAMMRKNGPDAENGSGTVNK 545

RESULT 3  
US-09-828-313-38  
; Sequence 38, Application US/09828313  
; Patent No. US20020059662A1  
; GENERAL INFORMATION:  
; APPLICANT: COSTA e SILVA, OSWALDO DA  
; APPLICANT: BOHNERT, HANS J.  
; APPLICANT: THIELEN, NOCHA VAN  
; APPLICANT: CHEN, ROUYING  
; APPLICANT: SARRIA-MILLAN, RODRIGO  
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
; FILE REFERENCE: 16313-0032  
; CURRENT APPLICATION NUMBER: US/09/828,313  
; PRIOR APPLICATION NUMBER: 60/196,001  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 597  
; TYPE: PRT  
; ORGANISM: Physcomitrella patens  
US-09-828-313-38

Query Match 32.7%; Score 849; DB 10; Length 597;  
Best Local Similarity 36.9%; Pred. No. 1.7e-52;  
Matches 203; Conservative 92; Mismatches 163; Indels 92; Gaps 14;  
Qy 5 PNPRPESNTVLPY-----QTPR----- 21  
Db 62 PSRPHSAGPLPHTSSPAPSTPRNIFKRPPEPPSPAKHIQSSLVKRGHAKPKEGGAIP 121  
Qy 22 -----LRDH-----YLLGKLGQGGFTYLTCTEKSANSY-----ACKSIP 58  
Db 122 EAVDGEKPLDKHFGVHKNFATKYLGEHVEGRGHGHT--CYAKVRKEHKGQAVAVKILS 179  
Qy 59 KRKLVCREDYEDVWREIQMHLSHPNVRAIKGTYESDVFIHMEVCEGGLFDRIVS 118  
Db 180 KAKMTTAAIATEDVGRVKILKALTGHQNLVRFYDSCEDHLNVIWMLCEGGLDRILS 239  
Qy 119 K-GHFSREAVKLIKTLGVVEACHSLGVWHRDLKPNFLPDSPKDDAKLKATDFGLSVF 177  
Db 240 RGGYSEEDAKVVRVRLSVVAFCHLQGVVHRDLKPNFLFTTKDEYTAQLKADIFGLSDF 239  
Qy 178 YKPGQYLYDVVGSYVYVAPVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQ 237  
Db 300 IKPDERLNDIVGSAYVYVAPVLHRLYSMEADVMSIGVITYILLGSRPFWARTESGIFRA 359  
Qy 238 ILQGLKDFKSDPMTTISEAAKDLIYKMLERSPKKRISEAHEALCHPWIIVDEQAAPDKPLDP 297  
Db 360 VLKADPSFEAPWPSISPEAKDFVRLLNKKMRKMTAAQALTPWIRSNV--KIFLDI 417  
Qy 298 AVLRLKQFSOMNKKKVALRVIAERLSEEEIGGLKELFKMTDNTSNTITFEELKAGLR 357  
Db 418 LVYRLVRNLRASSMRKAALKALSALTDETFVLTQFMLLEPSNNGRVTFENFROALL 477  
Qy 358 RVGSELM-ESEIKSLMDAADINDSGTIDYGEFFLAATLHMNMREBILVAAPSDPD 412  
Db 478 KNSTAMKSRVFEILSEMDGLHFKKNDGFSFCAAAISVLQLEATERWEQHARAAYDIFE 537  
Qy 413 KDGSYITIDELQSACTEFLGCD-TPLDMDMIKEIDLNDGKIDFSEFTAMMRKGDG 468  
Db 538 KEGNRVYIPDEL---AKENGLAPNVPAQVFLDWIRQ-----SDGRLSFTGTKLH----- 585  
Qy 469 GRSETVMKNL 473  
Db 586 GISRAIKNL 595

```

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match 31.9%; Score 826; DB 10; Length 625;
Best Local Similarity 40.8%; Pred. No. 7,3e-51;
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;

QY 26 YLGGKLGQGGTTLCTEKS---TSANYACKSPKPKLVCREDEYEDVWREIQIMHLS 82
DB 174 YDLGKEVGRGHFGHTCSAVVKKGEHKGHTVAVKIISKAKMTTAISIEDVRREVTKLKALS 233
QY 83 EHENVVRIGKTVEDSVFVHVMVEVCEGELFDRIYSK-GHFSEREA VKLIKTILGVREAC 141
DB 234 GHNLVRFYDACEALNVYIMVELCEGELLDRILARGRYTEEDAKALIIVILSVAF 293
QY 142 HSLGVNHRDLKPNFLFDSPKDADKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKK 201
DB 294 HLQGVNHRDLKPNFLFTRDSAPMKLIDFGLSDPIRDPERLNDIVGSAYVVAPEVLHR 353
QY 202 CYCPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDKSDPWTISEAAKOLI 261
DB 354 SYSMEADINSGVITYILLCSGRPFWARTESGIFRSVLRADPNFDDSPSPSVAEAKDFV 413
QY 262 YKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIKMALRVIA 321
DB 414 KRFENKDYRKMTAVQALTFPWLDRDQR--QIPDLILFRLVKQYLRATPLKRLALKALS 471
QY 322 ERLSBEIIGGLKELFKMIDTNSGTTFPEELKAGLKRVSGLM-ESEIKSLMDAADIDNS 380
DB 472 KALSEDELLYRLQFKLLE-PRDGFVSLDNFTALTRYSTDAMRESRVLEFQHALEPLAY 530
QY 381 GTDYGEBLAATL---HMNMKMER-EELVAAFSDFDKGSGYITIDELQSACTEFLGCDT 436
DB 531 RKVDFEFCAAISPYQLEALERWEEIAGTAFQHFQEGNVRISVEEL---AQELNLA 587
QY 437 P---LDDMIKEIDLDNDGKIDFSEFTAMM 462
DB 588 HYSIVQDWIRK---SDGKLNFLGFTKFL 612

RESULT 6
US-09-854-731-19
; Sequence 19, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-854-731-19

Query Match 30.9%; Score 800; DB 10; Length 576;
Best Local Similarity 38.1%; Pred. No. 4.5e-49;
Matches 177; Conservative 94; Mismatches 171; Indels 22; Gaps 10;

QY 25 HYLGGKLGQGGTTLCTEKSAN----YACKSIPKRLVCREDEYEDVWREIQIMH 79
DB 122 HYEDGVEGRGHFG--YTCSAKGKGLSGEVAVKVIPSCKMTTALIEDVRSREVLMR 179

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match 32.0%; Score 829; DB 10; Length 623;
Best Local Similarity 40.6%; Pred. No. 4.5e-51;
Matches 183; Conservative 87; Mismatches 155; Indels 26; Gaps 11;

QY 26 YLGGKLGQGGTTLCTEKSANY-----ACKSIPKRLVCREDEYEDVWREIQIMH 80
DB 172 YELGKEVGRGHFGHT--CSAVVKKGEYKQGTAVKIIAKAKMTTAISTEDVRREVTKILRA 229
QY 81 LGEHPNVRIGKTVEDSVFVHVMVEVCEGELFDRIYSK-GHFSEREA VKLIKTILGVVE 139
DB 230 LSGHNLVRFYDACEGLNVYIMVELCEGELLDRILARGRYTEEDAKAIVVQILSVVA 289
QY 140 ACHSLGVNHRDLKPNFLFDSPKDADKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 199
DB 290 FCHLQGVNHRDLKPNFLFTRDENAPMKLIDFGLSDPIRDPERLNDIVGSAYVVAPEVL 349
QY 200 KCYCPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDKSDPWTISEAAKD 259
DB 350 HRSYSMEADINSGVITYILLCSGRPFWARTESGIFRSVLRADPNFDDSPSPSVAEAKD 409
QY 260 LIYKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIKMALRV 319
DB 410 FVRRFLNKDYRKMTAVQALTFPWLDRDQR--QIPDLILFRLVKQYLRATPLKRLALK 467
QY 320 IAERLSBEIIGGLKELFKMIDTNSGTTFPEELKAGLKRVSGLM-ESEIKSLMDAADID 378
DB 468 LSKALREDELLYRLQFKLLE-PRDGFVSLDNFTALTRYSTDAMRESRVLEFQHALEPL 526
QY 379 NSGTIDYGEFLAATL---HMNMKMER-EELVAAFSDFDKGSGYITIDELQSACTEFLG 434
DB 527 AYRRMDPEFCAAISPYQLEALERWEEIAGTAFQHFQEGNVRISVEEL---AQELNLA 583
QY 435 DTP---LDDMIKEIDLDNDGKIDFSEFTAMM 462
DB 584 PTHYSIVQDWIRK---SDGKLNFLGFTKFL 610

RESULT 5
US-09-854-731-18
; Sequence 18, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998

```

```

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match 31.9%; Score 826; DB 10; Length 625;
Best Local Similarity 40.8%; Pred. No. 7,3e-51;
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;

QY 26 YLGGKLGQGGTTLCTEKS---TSANYACKSPKPKLVCREDEYEDVWREIQIMHLS 82
DB 174 YDLGKEVGRGHFGHTCSAVVKKGEHKGHTVAVKIISKAKMTTAISIEDVRREVKKLKALS 233
QY 83 EHENVVRIGKTVEDSVFVHVMVEVCEGELFDRIYSK-GHFSEREA VKLIKTILGVREAC 141
DB 234 GHNLVRFYDACEALNVYIMVELCEGELLDRILARGRYTEEDAKAIIVOLISVWAF 293
QY 142 HSLGVNHRDLKPNFLFDSPKDADAKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKK 201
DB 294 HLQGVNHRDLKPNFLFTRDSAPMKLIDFGLSDFIRPDERLNDIVGSAYVVAPEVLHR 353
QY 202 CYCPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDKSDPWTISEAAKOLI 261
DB 354 SYSMEADINSGVITYILLCGSRPFWARTESGIFRSVLRADPNFDDSPSPSVAEAKDFV 413
QY 262 YKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLRSRLKQFSQMNKIKMALRVIA 321
DB 414 KRFENKDYRKMTAVQALTFPWLDRDQR--QIPDLILFRLVKQYLRATPLKRLALKALS 471
QY 322 ERLSBEIIGGLKELFKMIDTNSGTTFPEELKAGLKRVGSELM-ESEIKSLMDAADIDNS 380
DB 472 KALSEDELLYRLQFKLLE-PRDGFVSLDNFRFTALTRYSTDAMRESRVLEFQHALEPLAY 530
QY 381 GTDYGEBLAATL---HMNMKMER-EELVAAFSDFDKDGSYITIDELQSACTEFLGCDT 436
DB 531 RKVDFEFCAAISPYQLEALERWEEIAGTAFQHFQEGNVRISVEEL---AQELNLA 587
QY 437 P---LDDMIKEIDLDNDGKIDFSEFTAMM 462
DB 588 HYSIVQDWIRK---SDGKLNFLGFTKFL 612

RESULT 6
US-09-854-731-19
; Sequence 19, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-854-731-19

Query Match 30.9%; Score 800; DB 10; Length 576;
Best Local Similarity 38.1%; Pred. No. 4.5e-49;
Matches 177; Conservative 94; Mismatches 171; Indels 22; Gaps 10;

QY 25 HYLGGKLGQGGTTLCTEKSAN-----YACKSIPKPKLVCREDEYEDVWREIQIMH 79
DB 122 HYEIDGVEGRGHFG--YTCSAKGKGLKGOEVAVKVIPSCKMTTALIEDVRSREVLMR 179

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18

Query Match 32.0%; Score 829; DB 10; Length 623;
Best Local Similarity 40.6%; Pred. No. 4.5e-51;
Matches 183; Conservative 87; Mismatches 155; Indels 26; Gaps 11;

QY 26 YLGGKLGQGGTTLCTEKSANY-----ACKSIPKPKLVCREDEYEDVWREIQIMH 80
DB 172 YELGKEVGRGHFGHT--CSAVVKKGEYKQGTAVKIIAKAKMTTAISTEDVRREVKKILRA 229
QY 81 LGEHPNVRIGKTVEDSVFVHVMVEVCEGELFDRIYSK-GHFSEREA VKLIKTILGVVE 139
DB 230 LSGHNLVRFYDACEGLNVYIMVELCEGELLDRILARGRYTEEDAKAIIVVQILSVVA 289
QY 140 ACHSLGVNHRDLKPNFLFDSPKDADAKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 199
DB 290 FCHLQGVNHRDLKPNFLFTRDENAPMKLIDFGLSDFIRPDERLNDIVGSAYVVAPEVL 349
QY 200 KCYCPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDKSDPWTISEAAKD 259
DB 350 HRSYSMEADINSGVITYILLCGSRPFWARTESGIFRSVLRADPNFDDSPSPSVAEAKD 409
QY 260 LIYKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLRSRLKQFSQMNKIKMALRV 319
DB 410 FVRRFLNKDYRKMTAVQALTFPWLDRDQR--QIPDLILFRLVKQYLRATPLKRLALKAL 467
QY 320 IAERLSBEIIGGLKELFKMIDTNSGTTFPEELKAGLKRVGSELM-ESEIKSLMDAADID 378
DB 468 LSKALREDELLYRLQFKLLE-PRDGFVSLDNFRFTALTRYSTDAMRESRVLEFQHALEPL 526
QY 379 NSGTIDYGEFLAATL---HMNMKMER-EELVAAFSDFDKDGSYITIDELQSACTEFLGJC 434
DB 527 AYRRMDPEFCAAISPYQLEALERWEEIAGTAFQHFQEGNVRISVEEL---AQELNLA 583
QY 435 DTP---LDDMIKEIDLDNDGKIDFSEFTAMM 462
DB 584 PTHYSIVQDWIRK---SDGKLNFLGFTKFL 610

RESULT 5
US-09-854-731-18
; Sequence 18, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998

```

QY 80 HLEHNPVRIKGTEDSVFVHIVMEVCEGGELFDRIYVK-GHSEAEVXLIKTILGV 138  
DB 180 ALTGKRLVQVDAFEDDENYVIMELCKGGELDKILQGGKYSSEDAKVMQILSV 239  
QY 139 EACSHGVNHRDLKPNFLDGPDKDAKDKATDFGLSVFYKGOYLYDVWGSPPYVAPEV 198  
DB 240 AYCHLQGVHRLDKPNFLFSTKDETSPLKALIDFGLSDVVKPDERLNDIVGSAYYVAPEV 299  
QY 199 LKCYGPEIDVWAGVILYLLSGVPPFAETESGIFRQILQGLDEKSDPWTISEAAK 258  
DB 300 LHRTYGTADWMSIGVIAYILLGSGRPFVARTESGIFRAVLKAEFNEAPMPSLPEAV 359  
QY 259 DLIVMLERSPKKRIKAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKMALR 318  
DB 360 DFVKRLNKKYRKLTAQAALCHPLVGSHEL-KIPSDMIIVKLKVYIMTSLRKSALA 418  
QY 319 VIAERLEEIGGKELFKWIDTDSNGTTFEBLKAGLKVGSSELM-BSEIKSLMDAADI 377  
DB 419 ALAKTLVPOLAVLREQFTLLGFSKNGYISMQNYKTAILKSTDKMKSRRVDFVHMISC 478  
QY 378 DNSGTIDYGEFLAATLHMKNVER---EELVAAFDFDKGSGYITIDELQSACTEFL 433  
DB 479 LOYKGLDFEFECASALSVQLEAMETWEQHARRAYELFEKDGNRPMIBELAS---ELGL 535  
QY 434 -CDTPLDDMTKIBDLNDGKIDSEFTAMRMKGGVGRSRTMK 476  
DB 536 GPSVPEVHVQLQDWIRHSDGKLSFLGFRLLH---GVS-SRTLOK 575  
RESULT 7  
US-09-935-464-36  
; Sequence 36, Application US/09935464  
; Publication No. US20030027153A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyer, Joanne  
; APPLICANT: Barrington-Martin, Rory  
; APPLICANT: Parker, Alexander  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA  
; FILE REFERENCE: 3322/1H702 US1  
; CURRENT APPLICATION NUMBER: US/09/935,464  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: US 09/757,300  
; PRIOR FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: Patent version 3.0  
; SEQ ID NO 36  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-464-36  
Query Match 22.7%; Score 587.5; DB 9; Length 317;  
Best Local Similarity 41.6%; Pred. No. 2.1e-34;  
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;  
GENERAL INFORMATION:  
APPLICANT: Bandaru, Rajasekhar  
TITLE OF INVENTION: 68730 and 69112, Protein Kinase  
Molecules and Uses Therefor  
FILE REFERENCE: MEI2000-521P1R(M)  
CURRENT APPLICATION NUMBER: US/10/024,036B  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/258222  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 357  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-024-036B-2

QY 257 AKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKK 314  
DB 239 AKDFIRHLMKDPKRFTECQALQHPWIAGDTAL-DKNTHQSVSEQIKKNFAKSKWKQ 295  
RESULT 8  
US-09-817-181-4  
; Sequence 4, Application US/09817181  
; Patent No. US20020142427A1  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV, Gennady et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01189  
; CURRENT APPLICATION NUMBER: US/09/817,181  
; CURRENT FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Human  
US-09-817-181-4  
Query Match 22.7%; Score 587.5; DB 10; Length 370;  
Best Local Similarity 41.6%; Pred. No. 2.5e-34;  
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;  
GENERAL INFORMATION:  
APPLICANT: Bandaru, Rajasekhar  
TITLE OF INVENTION: 68730 and 69112, Protein Kinase  
Molecules and Uses Therefor  
FILE REFERENCE: MEI2000-521P1R(M)  
CURRENT APPLICATION NUMBER: US/10/024,036B  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/258222  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 357  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-024-036B-2  
Query Match 21.4%; Score 554; DB 9; Length 357;  
Best Local Similarity 37.1%; Pred. No. 5.5e-32;  
GENERAL INFORMATION:  
APPLICANT: Bandaru, Rajasekhar  
TITLE OF INVENTION: 68730 and 69112, Protein Kinase  
Molecules and Uses Therefor  
FILE REFERENCE: MEI2000-521P1R(M)  
CURRENT APPLICATION NUMBER: US/10/024,036B  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/258222  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 357  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-024-036B-2

Matches 117; Conservative 66; Mismatches 120; Indels 12; Gaps 6;

QY 32 LQGGGFGTTLCTEKSTANYACKSIPKRLKLVCEDEDVWREIQIMHLSHEPNVRIK 91  
 DB 29 LQGAPEVLAEEKATGKLFACIKPKALGKE--SSINEIAVURKI-KHENIVALE 85

QY 92 GTYDSVFVHMEVCEGELFDRIVSKGHFSEAEVAVLKIITLGVVEACHSLGVMRDL 151  
 DB 86 DYESPNHLYVMQLVSGGELFDRIVEKGFVTEKDASTLIRQLVDVAVYLRMGIVHRDL 145

QY 152 KPENFLPSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYVVAPEVL-KKCYGPELDVW 210  
 DB 146 KPENLVLYXSQDEESKIMSDRGLSKQKGGKGVMTAGTGGYVAPEVLAQKPYSKAVDCW 205

QY 211 SAGVILYLLSGVPPFMAETSGIFRQTLQGLKDFKDPNPTISEAAKDIYIKMLERSPK 270  
 DB 206 SIGVIAYILLGYPFFYDENDSKLFEQILKAEYBFDSPYWDIDSDAKDFIRNLMEKDPN 265

QY 271 KRISAHEALCHPWIVDQAAKPKDPAVLRL-KQPSQNMKIKKMLRVIABEELSEEEI 329  
 DB 266 KRYTCEAARHPWIAQDTAL-NKNIHESVSAQIRKNFAKSKWQAFNATAVVRHMRKLHL 324

QY 330 GGLKELFKMIDTNS 344  
 DB 325 G-----SSLDSNA 333

RESULT 10  
 JS-10-096-960-4  
 ; Sequence 4, Application US/10096960  
 ; Patent No. US20020132325A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YE, Jane et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; FILE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001158DIV  
 ; CURRENT APPLICATION NUMBER: US/10/096,960  
 ; CURRENT FILING DATE: 2002-03-14  
 ; PRIOR APPLICATION NUMBER: 09/800,960  
 ; PRIOR FILING DATE: 2001-03-08  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 556  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-10-096-960-4

Query Match 21.0%; Score 543.5; DB 12; Length 556;  
 Best Local Similarity 37.0%; Pred. No. 5.2e-31;  
 Matches 120; Conservative 63; Mismatches 128; Indels 13; Gaps 5;

QY 21 RLQDHYLLKGLGOGFTTLYCTEKSTANYACKSIPKRLKLVCEDEDVWREIQIMH 80  
 DB 9 RFTDDYQLFEELKGAFSVVRCKVTSTQEYAAKIINTKLSAR-DHOKLEREARIC-R 66

QY 81 LSEHPNVVRIKTYEDSVFVHMEVCEGELFDRIVSKGHFSEAEVAVLKIITLGVVEA 140  
 DB 67 LLKHPNIVRLHDSISEGTHYLVFDLVTGGELEFEDIVAREYSEADASHCIHQULESNH 126

QY 141 CHSLGVNHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPYVVAPEVL 199  
 DB 127 IHQHDIVHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPYVVAPEVL 186

QY 200 KK-CYGEIDVMSAGVILYLLSGVPPFMAETSGIFRQTLQGLKDFKSDPWTISEAAK 258  
 DB 187 RKPYPKPDVIMACGVILLYLLSGVPPFMAETSGIFRQTLQGLKDFKSDPWTISEAAK 246

QY 259 DLIVKMLERSPKKRISAHEALCHPWIVDQAAKPKDPAVLRLKQPSQNMKIKKMLR 318  
 DB 247 NLINQMLTINPAKRITADQALKHPWVQCORSTVASMHRQETVECLRKFNARRKLGALT 306

QY 319 VI-----AERLSEEEIGGLK 333  
 DB 307 TMLVSRNFSAAKSLLNKKSGGVK 330

RESULT 11  
 US-09-935-464-3  
 ; Sequence 3, Application US/09935464  
 ; Publication No. US20030027153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meyer, Joanne  
 ; APPLICANT: Barrington-Martin, Rory  
 ; APPLICANT: Parker, Alexander  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA  
 ; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA  
 ; FILE REFERENCE: 3322/1H702 US1  
 ; CURRENT APPLICATION NUMBER: US/09/935,464  
 ; CURRENT FILING DATE: 2001-08-23  
 ; PRIOR APPLICATION NUMBER: US 09/757,300  
 ; PRIOR FILING DATE: 2001-01-09  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 460  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-935-464-3

Query Match 20.9%; Score 543; DB 9; Length 460;  
 Best Local Similarity 39.6%; Pred. No. 4.5e-31;  
 Matches 116; Conservative 62; Mismatches 107; Indels 8; Gaps 6;

QY 18 QTPRLRDHYLLKGLGOGFTTLYCTEKSTANYACKSIPKRLKLVCEDEDVWREIQI 77  
 DB 15 QTTIRKRTTFMEVGGGATSEVPLVQRITKGLFALKCIKSPAFRDSLEN--EIAV 71

QY 78 MHLSEHPNVVRIKTYEDSVFVHMEVCEGELFDRIVSKGHFSEAEVAVLKIITLGV 137  
 DB 72 LKKI-KHENIVTLEDIVESTTHYVLMQLVSGGELFDRILRGVYTEKDALVIQVLSA 130

QY 138 VEACHSLGVNHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPYVVAPE 197  
 DB 131 VKYLHENGIVHRDLKPENFLPSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPYVVAPE 189

QY 198 VL-KKCYGEIDVMSAGVILYLLSGVPPFMAETSGIFRQTLQGLKDFKSDPWTISEA 256  
 DB 190 VLAQKPYKAVDCHWSIGVITVILLGYPPEYETESKLFKIKEGYVEFSPFWDIDISE 249

QY 257 AKDLIVKMLERSPKKRISAHEALCHPWIVDQAAKPKDPAVL-LSRLKQPSQ 308  
 DB 250 AKDFTCHLEKDPNERYTCEKALSHPMI-DGNTALHRDIYPSVLSQIQKNFAK 301

RESULT 12  
 US-09-935-464-5  
 ; Sequence 5, Application US/09935464  
 ; Publication No. US20030027153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meyer, Joanne  
 ; APPLICANT: Barrington-Martin, Rory  
 ; APPLICANT: Parker, Alexander  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA  
 ; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA  
 ; FILE REFERENCE: 3322/1H702 US1  
 ; CURRENT APPLICATION NUMBER: US/09/935,464  
 ; CURRENT FILING DATE: 2001-08-23  
 ; PRIOR APPLICATION NUMBER: US 09/757,300  
 ; PRIOR FILING DATE: 2001-01-09  
 ; NUMBER OF SEQ ID NOS: 90  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 476  
 ; TYPE: PRT

```

; ORGANISM: Homo sapiens
US-09-935-464-5

Query Match      20.9%; Score 543; DB 9; Length 476;
Best Local Similarity 39.6%; Pred. No. 4.7e-31;
Matches 116; Conservative 62; Mismatches 107; Indels 8; Gaps 6;

QY 18 QPRLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIKPKLVCREDEDYVWREIQI 77
DB 15 QTNINRKTIFNEVLGSGAFSEVFLVQELTCKLPALKCIKSPAFRDSLEN---BIAV 71

QY 78 MHLSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHFSEBAVKLTKILGV 137
DB 72 LKKI-KHENIVTLEDIYESTHYLVNQLVSGGELFDRIILRGVYTERKASLVIAQQVLSA 130

QY 138 VEACHSLGVMHDLKPENFLDPSKDDAKLKDGLSVFYKPGQYLDVVGSPYYVAPE 197
DB 131 VKYLHENGIVHRLDKPENLLYLPENSIMINTDGLSKWEQNG-IMSTAGCTGYVAPE 189

QY 198 VL-KCYGPEIDVMSAGVLYILLSGVPPFMAETESGIFRQLQKLDKSDPWPMTISEA 256
DB 190 VLAQKPYSKAVDCWSIGVITYILLCGYPPEYETESKLPFKIKEGYEFESFPFWDISES 249

QY 257 AKOLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKLPDPAV-LSRLKQFSQ 308
DB 250 AKOFICHLLEKDPNERYTCEKALSHPWI-DGNTALHRDIYPSVLSIQIKNTAK 301

RESULT 13
US-10-096-960-2
; Sequence 2; Application US/10056960
; Patent No. US20020132325A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001158DIV
; CURRENT APPLICATION NUMBER: US/10/096,960
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/800,960
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-960-2

Query Match      20.8%; Score 539; DB 12; Length 565;
Best Local Similarity 39.0%; Pred. No. 1.1e-30;
Matches 115; Conservative 58; Mismatches 118; Indels 4; Gaps 4;

QY 21 RLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIKPKLVCREDEDYVWREIQIMHH 80
DB 9 RFTDDYQLFEELGKGFASVVRRCVKKTSTQCYAAKIINTKLSAR-DHQKLESEARIC-R 66

QY 81 LSEHPNVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHFSEBAVKLTKILGVWEA 140
DB 67 LKHNIVLHDSISEEGFHYLVFDLVLTGGLFEDIAREYSEADASHCIHQILSSVNH 126

QY 141 CHSLGVMHDLKPENFLDPSKDDAKLKDGLSVFYKPGQYLDVVGSPYYVAPEVL 199
DB 127 IHQHDIVHRLDKPENLLYLPENSIMINTDGLSKWEQNG-IMSTAGCTGYVAPEVL 186

QY 200 KK-CYGPETDVMASGVLYILLSGVPPFMAETESGIFRQLQKLDKSDPWPMTISEAK 258
DB 187 RKDPTGKPDVIMACGVILYILLGVFPFDEQHLVQIKAGAYDPPSPENDVTVPPEAK 246

QY 259 DLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKLPDPAVLSRLKQFSQNKIK 313
DB 247 NLINQMLTINPAKRITADQALKHPWVCQRSTVASMWHRQETVECLRFNARFKLK 301
```

```

; ORGANISM: Homo sapiens
US-09-817-181-2

Query Match      20.8%; Score 538.5; DB 10; Length 326;
Best Local Similarity 42.8%; Pred. No. 6.1e-31;
Matches 107; Conservative 53; Mismatches 87; Indels 3; Gaps 3;

QY 66 EDEYDVMREIQIMHLSHPNVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHFSE 125
DB 14 EDIRDIYDPRVLGTI-KHPNIVALDDIYESGCHLYLLIMQLVSGGELFDRIIVEKGFYTER 72

QY 126 EAVKLKTLILGVWEACHSLGVMHDLKPENFLDPSKDDAKLKDGLSVFYKPGQYLY 185
DB 73 DASRLIFQVLDAVKYLHDLGIVHRLDKPENLLYLSLDBDSKIMISDFGLSKMEDPGSVLS 132

QY 186 DVVGSPYYVAPEVL-KCYGPEIDVMSAGVLYILLSGVPPFMAETESGIFRQLQKLD 244
DB 133 TAGCTGYVAPEVLQAKPYSKAVDCWSIGVIAIYLLCGYPFYPDENAKLEFEQILKAEYE 192

QY 245 FKSDPWPMTISEAKOLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKLPDPAVLSRLK 304
DB 193 FDSYPWDDISDAKDFIRHLMKDPKFTCEQALQHPWIAGDTAL-DKNIHQSVSEQIK 251

QY 305 QFSQMNKIKK 314
DB 252 KNFAKSKWKQ 261

RESULT 15
US-09-771-161A-188
; Sequence 188; Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 188
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-188

Query Match      20.6%; Score 533.5; DB 10; Length 387;
Best Local Similarity 37.0%; Pred. No. 1.7e-30;
```

		Matches 115;	Conservative 53;	Mismatches 100;	Indels 43;	Gaps 7;
QY	32	LGQGGTGYLCTEKSTSNYACKSI-----PKRKLVCREDYEDVWREIQIMHLS	82			
DB	26	LGRGSSVVRRCIHKPTQOYAVKVIDVTGGSGFPEE---VRELREATLKEVDILRKVS	82			
QY	83	EHNVRIRIKGTYESDVVHVIMVEVCEGGELFDRIVSKGHFSERBAVKLIKILGWVWACH	142			
DB	83	CHNIIQLKDTYETNTFFFLVFDLMKRGELFDYLTSEKETRKIMRALLEVICTLH	142			
QY	143	SLGVHRDLKPNFLPDSKDKAKLKDGLSVFYKPGQYLYDVVGSPPYVAVPEVLKCC	202			
DB	143	KLNIHRDLKPNILLD---DNMNIKLTDFGFCQLEPGERLREVCSTPSYLAPEII-EC	198			
QY	203	-----YGPEIDVMSAGVILYILLSGVPPFWAETESGIFRQILQGLDKLDFKSDPWPTIS	254			
DB	199	SMNEDHFGYKGVDMSTGVIMYTLLAGSPFWHRKQMLMIMSGNYQFGSPENDDYS	258			
QY	255	EAAKDLIYKMLERSPKKRISAHEALCHP-----WIVDEQAAPDKPLDPAVLSRLKQFSQMN	310			
DB	259	DTVKDLVSRFLVVQPQNRYTABEALAHPPFOQLVEE-----VRHFSPRG	303			
QY	311	KIKKMLRVIA	321			
DB	304	KFKVIALTVLA	314			

Search completed: February 13, 2003, 21:18:42  
Job time : 20 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 21:04:42 ; Search time 38 Seconds

(without alignments)  
1252.277 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KLNLFNIADAFGVDGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2593	100.0	495	1 S46284	calcium-dependent
2	2458	94.8	501	2 G85097	hypothetical prote
3	2030	78.3	490	2 T08873	calcium-dependent
4	1944	75.0	508	1 A43713	calcium-dependent
5	1847.5	71.2	490	1 S71776	calcium-dependent
6	1752	67.6	492	1 T03271	calcium-dependent
7	1751	67.5	487	1 S71770	calcium-dependent
8	1745	67.3	554	1 T03263	calcium-dependent
9	1742	67.2	556	2 T06126	calcium-dependent
10	1731	66.8	544	2 D84550	probable calmoduli
11	1724	66.5	610	1 A49082	calcium-dependent
12	1709.5	65.9	573	2 T09940	calcium-dependent
13	1700.5	65.6	484	2 T05650	calcium-dependent
14	1672.5	64.5	639	1 T02784	calcium-dependent
15	1640.5	63.3	593	2 H84810	probable calcium-d
16	1630	62.9	451	2 S56717	calcium-dependent
17	1586	61.2	542	1 S56651	calcium-dependent
18	1484.5	57.3	540	1 T01989	calcium-dependent
19	1482	57.2	531	2 D85059	probable calcium d
20	1482	57.2	533	1 S56652	calcium-dependent
21	1480	57.1	531	1 T02993	calcium-dependent
22	1453.5	56.4	521	2 G96543	calcium-dependent
23	1462	56.4	529	1 S71774	calcium-dependent
24	1460.5	56.3	513	1 T02259	calcium-dependent
25	1460	56.3	534	1 JC1515	calcium-dependent
26	1456.5	56.2	538	2 T08874	calcium-dependent
27	1449	55.9	554	2 T05476	calcium-dependent
28	1437.5	55.4	465	1 T03024	calcium-dependent
29	1432.5	55.2	532	2 T14335	protein kinase, ca

30	1431	55.2	514	2 T10938	calcium-dependent
31	1381	53.3	545	2 H86322	calcium-dependent
32	1367.5	52.7	493	1 S46283	calcium-dependent
33	1363	52.6	541	2 F96776	hypothetical prote
34	1361	52.5	553	1 T02139	calcium-dependent
35	1356.5	52.3	520	2 F85059	probable calcium d
36	1325.5	51.1	560	2 T46189	calcium-dependent
37	1324.5	51.1	425	2 S17759	protein kinase, ca
38	1313.5	50.7	533	1 S71778	calcium-dependent
39	1287.5	49.7	520	2 C84774	probable calcium-d
40	1280.5	49.4	530	2 A84847	probable Ca2+ depe
41	1238.5	47.8	582	2 E84721	probable calcium-d
42	1229.5	47.4	575	2 C85059	calcium-dependent
43	1225.5	47.3	503	2 T51156	calcium-dependent
44	1176.5	45.4	591	2 S54788	calcium-stimulated
45	1056.5	40.7	571	2 T00835	calcium-dependent

ALIGNMENTS

RESULT 1

S46284  
calcium-dependent protein kinase (EC 2.7.1.1-) 2 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 16-Jun-2000  
C:Accession: S46284  
R:Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shinozaki, M. Gen. Genet. 244, 331-340, 1994  
A:Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by drought  
A:Reference number: S46283; MUID:94359455; PMID:8078458  
A:Accession: S46284  
A:Molecule type: mRNA  
A:Residues: 1-495 <URA>  
A:Cross-references: EMBL:D21806; NID:G1235717; PIDN:BA04830.1; PID:G604881  
C:Genetics:  
A:Gene: CDPK2  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki  
C:Keywords: ATP; calcium binding; pf hand; phosphotransferase; serine/threonine-specifi  
F:24-284/Domain: protein kinase homology <KIN>  
F:32-40/Region: protein kinase ATP-binding motif  
F:327-359/Domain: calmodulin repeat homology <EF1>  
F:363-395/Domain: calmodulin repeat homology <EF2>  
F:399-431/Domain: calmodulin repeat homology <EF3>  
F:433-465/Domain: calmodulin repeat homology <EF4>  
F:55/Active site: Lys #status Predicted

Query Match 100.0%; Score 2593; DB 1; Length 495;  
Best Local Similarity 100.0%; Pred. No. 1.6e-99;  
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	METKPNRRPSNTVLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPIKR	60
Db	1	METKPNRRPSNTVLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTSANVACKSIPIKR	60
Qy	61	KLVCREDYEDVWREIQIMHLSHPNVRIKITYEDSVFVHIVMEVCEGGEFLDRIVSKG	120
Db	61	KLVCREDYEDVWREIQIMHLSHPNVRIKITYEDSVFVHIVMEVCEGGEFLDRIVSKG	120
Qy	121	HFSEREAVKLIKITLGVWACHSLGVMHRDLKPNFLDPSPKDDAKLKATDFGLSVFYKP	180
Db	121	HFSEREAVKLIKITLGVWACHSLGVMHRDLKPNFLDPSPKDDAKLKATDFGLSVFYKP	180
Qy	181	GQVLYDVVGSPYYVAPEVLKCKYCPEDVMSAGVILYLLSGVPPFWAETESGIFRQILQ	240
Db	181	GQVLYDVVGSPYYVAPEVLKCKYCPEDVMSAGVILYLLSGVPPFWAETESGIFRQILQ	240
Qy	241	GKLDPKSDPPTTISEAAKDLIYKMLERSPKRISAEALCHPWIDEQAAPKPLDPAVL	300
Db	241	GKLDPKSDPPTTISEAAKDLIYKMLERSPKRISAEALCHPWIDEQAAPKPLDPAVL	300
Qy	301	SRLKQFSQMNKIKMALRVAERLSSEETGGELKELFMIDTNSGTTITFEELKAGIKRVG	360

Db 301 SRLKQFQOMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKEVG 360  
 Qy 361 SELMESIKSLMDAADIDNSGTTIDYGEFLAATLHNMKEREELVAAESDPKDGSGYIT 420  
 Db 361 SELMESIKSLMDAADIDNSGTTIDYGEFLAATLHNMKEREELVAAESDPKDGSGYIT 420  
 Qy 421 IDELQSACTEFLGCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGRSRRTMMKNLNF 480  
 Db 421 IDELQSACTEFLGCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGRSRRTMMKNLNF 480  
 Qy 481 NIADAFGVDGEKSDD 495  
 Db 481 NIADAFGVDGEKSDD 495  
 RESULT 2  
 C85097  
 C:Species: Arabidopsis thaliana [imported] - Arabidopsis thaliana  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 23-Mar-2001  
 C:Accession: G85097  
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999  
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10611798  
 A:Accession: G85097  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-501 <STO>  
 A:Cross-references: GB:NC\_001268; NID:g2767652; PIDN:CAB78080.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4g09570  
 A:Map position: 4  
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
 C:Keywords: EF hand  
 Query Match 94.8%; Score 2458; DB 2; Length 501;  
 Best Local Similarity 94.8%; Pred. No. 1.6e-84;  
 Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;  
 Qy 4 KPNRRPNTVLVPTQTPRLRHYLLGKLGQGGTGYLCTEKSSTANYACKSIPIPRKLV 63  
 Db 3 KPNRRPNSVLPVETPLRHYLLGKLGQGGTGYLCTEKSSTANYACKSIPIPRKLV 62  
 Qy 64 CREDYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGEFLDRIIVSKGHFS 123  
 Db 63 CREDYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGEFLDRIIVSKGCF 122  
 Qy 124 EREAVKLITLGVVEACHSLGWVHRDLKPNFLDPGPKDDAKLKATDFGLSVFPKQY 183  
 Db 123 EREAAKLITLGVVEACHSLGWVHRDLKPNFLDPGSPDDAKLKATDFGLSVFPKQY 182  
 Qy 184 LYDVVGSPPYVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGL 243  
 Db 183 LYDVVGSPPYVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGI 242  
 Qy 244 DFKSDPMTISEAAKDLTIYMLERSPKKRISAHEALCHPWIIVDEQAAPDKLPDPAVL 303  
 Db 243 DFKSDPMTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIIVDESHAAPDKLPDPAVL 302  
 Qy 304 KQFSQMKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKEVGSEL 363  
 Db 303 KQFSQMKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKEVGSEL 362  
 Qy 364 MESEIKSLMDAADIDNSGTTIDYGEFLAATLHNMKEREELVAAESDPKDGSGYITIDE 423  
 Db 363 MESEIKSLMDAADIDNSGTTIDYGEFLAATLHNMKEREELVAAESDPKDGSGYITIDE 422  
 Qy 424 LQSACTEFLGCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGRSRRTMMKNLNF 483  
 Db 423 LQSACTEFLGCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGRSRRTMMKNLNF 482  
 Qy 484 DAFGVDG-----EKSSD 495

Db 483 EAFGVEDTSTAKSDD 498  
 RESULT 3  
 T08873  
 calcium-dependent protein kinase (EC 2.7.1.1-) beta - soybean  
 C:Species: Glycine max (soybean)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jan-2000  
 C:Accession: T08873  
 R:Lee, J.Y.; Yoo, B.C.; Harmon, A.C.  
 submitted to the EMBL Data Library, September 1996  
 A:Reference number: Z16505  
 A:Accession: T08873  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-490 <IEE>  
 A:Cross-references: EMBL:U69173; NID:g2501763; PID:g2501764  
 C:Genetics:  
 A:Gene: CDPK beta  
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki  
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specifi  
 F;22-282/Domain: protein kinase homology <kin>  
 F;30-38/Region: protein kinase ATP-binding motif  
 F;324-356/Domain: calmodulin repeat homology <EPH>  
 F;53/Active site: Lys #status Predicted  
 Query Match 78.3%; Score 2030; DB 2; Length 490;  
 Best Local Similarity 81.1%; Pred. No. 1e-68;  
 Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;  
 Qy 14 VLPYQTPRLRHYLLGKLGQGGTGYLCTEKSSTANYACKSIPIPRKLVCREYEDVWR 73  
 Db 12 VLPYQTPARLDHYVLGKLGQGGTGYLCTHKVTGKLYACKSIPIPRKLMCOEDYDDVWR 71  
 Qy 74 BIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGEFLDRIIVSKGHFSREAVKLIT 133  
 Db 72 BIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGEFLDRIIVSKGHFSREAAKLIT 131  
 Qy 134 ILGVVEACHSLGWVHRDLKPNFLDPGPKDDAKLKATDFGLSVFPKQYLYDVVGSPPY 193  
 Db 132 IVGVVEACHSLGWVHRDLKPNFLDTPGDEAQMKTDFGLSVILQARQAFHDVVGSPY 191  
 Qy 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKSPDPWPTI 253  
 Db 192 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETAGIFRQILNGDLDFVSEWPPI 251  
 Qy 254 SEAAKDLTIYMLERSPKKRISAHEALCHPWIIVDEQAAPDKLPDPAVLSELKQFSQMKIK 313  
 Db 252 SENAKELVKQMLDRDPKKRISAHEVLCNPVVDQ-IAPDKPLDSAVLTRKXFSAMNKLK 310  
 Qy 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVSSELMSEIKSLMD 373  
 Db 311 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKEGUKSVGSNLMSEIKSLME 370  
 Qy 374 AADINSGTIDYGEFLAATLHNMKEREELVAAESDPKDGSGYITIDELQSACTEPGL 433  
 Db 371 AADINSGTIDYGEFLAATLHNMKEREELVAAESDPKDGSGYITIDELQSACTEPGL 430  
 Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMMKNLNFNIADAFG 488  
 Db 431 GDVHLEMIKEIDQNDGRIDYAEFAAMKKGDPNMGSRRTMKGNLNFNIADAFGM 486  
 RESULT 4  
 A43713  
 calcium-dependent protein kinase (EC 2.7.1.1-) - soybean  
 C:Species: Glycine max (soybean)  
 C:Date: 03-Mar-1993 #sequence\_revision 14-Jul-1994 #text\_change 11-Jun-1999  
 C:Accession: A43713  
 R:Harper, J.F.; Sussman, M.R.; Schaller, G.B.; Putnam-Evans, C.; Charbonneau, H.; Harm  
 Science 252, 951-954, 1991  
 A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmod

A:Reference number: A43713; MUID:91240279; PMID:1852075

A:Accession: A43713

A:Molecule type: mRNA

A:Residues: 1-508 <HNA>

A:Cross-references: EMBL:M64987; NID:G169930; PID:AAB0806.1; PID:G169931

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F:32-292/Domain: protein kinase homology <KIN>

F:40-48/Region: protein kinase ATP-binding motif

F:335-367/Domain: calmodulin repeat homology <EF1>

F:371-403/Domain: calmodulin repeat homology <EF2>

F:407-439/Domain: calmodulin repeat homology <EF3>

F:441-473/Domain: calmodulin repeat homology <EF4>

F:63/Active site: Lys #status predicted

Query Match 75.0%; Score 1944; DB 1; Length 508;

Best Local Similarity 77.7%; Pred. No. 1.6e-65;

Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;

QY 14 VLPYQTPRLRDHYLLGKLGQCGQGTTLCTEKSTSYACKSPKRLKVCREDYEDVWR 73

DB 22 VLPQRTQNIREVVEVGRKLGQCGQGTTFCTRRASGGKPAKSPKRLCKEDYEDVWR 81

QY 74 EQIMHHLSEHPNVRKGTYSVFIHVEVCEGGLFDRIVSKGHFSREAVKLKT 133

DB 82 EQIMHHLSEHANVVRIGTYEDSTAVHLVWELCEGGLFDRIVQKGYHSEQAARLKT 141

QY 134 ILGVVACHSLGWHRDLKPNFLFDSPKDPAKATDGLSVFVKPGQYLDYVVGSPYY 193

DB 142 IVEVVEACHSLGWHRDLKPNFLFDTIDEDAKATDGLSVFVKPGESCDVVGSPYY 201

QY 194 VAPVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQKLFKDPPTI 253

DB 202 VAPVLRLKLYGPESDVMSAGVILYLLSGVPPFWAETSGIFRQILQKLFKDPPTI 261

QY 254 SEAAKLLIYKMLERSPKKISAEALCHPMIWEQAAPDKPLDPAVLRLKQFQSMKKIK 313

DB 262 SDSAKLLIYKMLDQNPKTALTAHEVLRHPIVDDNIADPKPLDSAVLSRLKQFSAMKLIK 321

QY 314 KQALRVIAERLSEETGGKELFKMIDTNSGTITTFEELKAGLRKVGSELMESEIKSLMD 373

DB 322 KQALRVIAERLSEETGGKELFKMIDTNSGTITTFEELKAGLRKVGSELMESEIKSLMD 381

QY 374 AADIDNSGTIDYGEFLAATLHNNKWEREILVAAPSDPKDQSGVITIDELQSACTEGL 433

DB 382 AADIDNSGTIDYGEFLAATLHNNKWEREILVAAPSDPKDQSGVITIDELQSACTEGL 441

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMVRKGD-GVGRSRTMMKXNFIADAFV 488

DB 442 DDIHDDMIKEIQDNDGQIDYGEFAAMVRKNGGIGR-RTWRKTL--NLRDALGL 494

RESULT 5

S71776

calcium-dependent protein kinase (EC 2.7.1.1) 9 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence revision 14-May-1999 #text\_change 18-Jun-1999

A:Accession: S71776; S71775; S71902; S71196

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, N.H.

Plant Mol. Biol. 30, 1259-1275, 1996

A:Title: Expression of three members of the calcium-dependent protein kinase gene family

A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71776

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-490 <HON>

A:Cross-references: EMBL:U20626

A:Accession: S71775

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-490 <HOF>

A:Cross-references: EMBL:U20388

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, N.H.; Tan, C.T.; Koh, C.C.; Chua, N.

submitted to the EMBL Data Library, February 1995

A:Description: Expression of the calcium-dependent protein kinase gene family in Arabid

A:Reference number: S71197

A:Accession: S71902

A:Molecule type: DNA

A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HON>

A:Cross-references: EMBL:U20626; NID:G836945; PID:AAA67657.1; PID:G836946

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, N.H.; Tan, C.T.; Koh, C.C.; Chua, N

submitted to the EMBL Data Library, January 1995

A:Description: Expression of the calcium dependent protein kinase gene family in Arabid

A:Reference number: S71196

A:Accession: S71196

A:Molecule type: mRNA

A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HON>

A:Cross-references: EMBL:U20388; NID:G836937; PID:AAA67653.1; PID:G836938

C:Genetics:

A:Gene: CDPK9

A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F:20-286/Domain: protein kinase homology <KIN>

F:223-365/Region: protein kinase ATP-binding motif

F:323-355/Domain: calmodulin repeat homology <EF1>

F:359-391/Domain: calmodulin repeat homology <EF2>

F:395-427/Domain: calmodulin repeat homology <EF3>

F:429-461/Domain: calmodulin repeat homology <EF4>

F:51/Active site: Lys #status predicted

Query Match 71.2%; Score 1847.5; DB 1; Length 490;

Best Local Similarity 73.5%; Pred. No. 5.6e-62;

Matches 355; Conservative 52; Mismatches 69; Indels 7; Gaps 2;

QY 1 METKNPRPNTVLPYQTPRLRDHYLLGKLGQCGQGTTLCTEKSTSYACKSPKXR 60

DB 1 VANKPRTT---WVLPYKTRNVEDNYFLGVLGQCGQGTTLCTHKOTGKLACKSPKXR 56

QY 61 KLVCREDYEDVWREIQIMHHLSEHPNVRKGTYSVFIHVEVCEGGLFDRIVSKG 120

DB 57 KLLCEDYEDVWREIQIMHHLSEHPNVRKGTYSVFIHVEVCEGGLFDRIVKRG 116

QY 121 HFSEBAVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDPAKATDGLSVFYKP 180

DB 117 HYSERBAKLIKTIIVGVVEACHSLGVWHRDLKPNFLFDSSEDEASLKATDGLSVFCTP 176

QY 181 GOYLDVWVSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQ 240

DB 177 GFAPSELVGSAYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQ 236

QY 241 GKLDPKSDPWPPTISAADKLIYKMLERSPKKIRSAHALCHPMIWEQAAPDKPLDPAVL 300

DB 237 GKLDPEINPWPSPISBSAKDLIKOMLESNPKKRLTAHQVLCHEPMTIVDDKVPKPLDCAV 296

QY 301 SRLKQFSQWNTKKQALRVIAERLSEETGGKELFKMIDTNSGTITTFEELKAGLRKVG 360

DB 297 SRLKQFSQWNTKKQALRVIAERLSEETGGKELFKMIDTNSGTITTFEELKAGLRKVG 356

QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHNNKWEREILVAAPSDPKDQSGVIT 420

DB 357 SELMESEIQELLRAADVDSEGTIDYGEFLAATLHNNKWEREILVAAPSDPKDQSGVIT 416

QY 421 IDELQSACTEFLGLCTPLDDMIKEIDLNDGKIDFSEFTAMVRKGDGVGRS---RTWMKN 477

DB 417 IEELQQAWEKFGINDSNLDEMIDKIQDNDGQIDYGEFAAMVRKNGGIGRRTWRNS 476

QY 478 LNF 480

DB 477 LNF 479

RESULT 6

T03271

calcium-dependent protein kinase (EC 2.7.1.1) 1 - maize

C:Species: Zea mays (maize)

C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 16-Jun-2000  
C/Accession: T03271  
R:Berberich, T.; Kusano, T.  
Mol. Gen. Genet. 254, 275-283, 1996  
A/Title: Cycloheximide induces a subset of low temperature-inducible genes in maize.  
A/Reference number: Z14873  
A/Accession: T03271  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-492 <BER>  
A/Cross-references: EMBL:D84408; PIDN:BAAL2338.1  
A/Experimental source: strain honey bantum  
A/Note: low temperature-inducible  
C/Genetics:  
A/Genes: CDPK1  
C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F/25-285/Domain: protein kinase homology <KIN>  
F/33-41/Region: protein kinase ATP-binding motif  
F/328-360/Domain: calmodulin repeat homology <EF1>  
F/364-396/Domain: calmodulin repeat homology <EF2>  
F/400-432/Domain: calmodulin repeat homology <EF3>  
F/434-466/Domain: calmodulin repeat homology <EF4>  
F/56/Active site: Lys #status predicted

Query Match 67.6%; Score 1752; DB 1; Length 492;  
Best Local Similarity 70.6%; Pred. No. 1.9e-58;  
Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;  
QY 13 TVLPYQTPRLRDHYLLGKLGOGQFGTTLCTEKSANSYACKSPKRLKVCREDYEDVW 72  
DB 14 SVLGHKTPNIRDDYALGRKLGOGQFGTTLCTELATGIDYACKSISKRLIKEDVDVR 73  
QY 73 REIQMHLSSEHPNVVRIRKGYEDSVFVHVMVECGEGELFDRIVSKGHFSERAVKLIK 132  
DB 74 REIQMHLSGHKNVVAIKGAYEDQVHVHVMELCAGGELFDRIIQRGHYSRKAALTR 133  
QY 133 TLGVVACHSLGWHRDLKPENFLPDSKDDAKLKTATDGLSVFKPGQYLYDVVGSPPY 192  
DB 134 IIVGVVACHSLGWHRDLKPENFLANRDDLSUKADFGLSVFFKPGQVTFDVVGSPPY 193  
QY 193 YVAPEVLKCKYGPIDVWSAGVILYLLSGVPPFWAETSGIFRQIQLOGKLDKSDPWPMT 252  
DB 194 YVAPEVLKSGVPAADVTAGVILYLLSGVPPFWAETQGGIFDAVLKGAIDFSDPWPV 253  
QY 253 ISEAAKOLIIYKMLERSPKKRISEAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKI 312  
DB 254 ISDSAKOLIREMLNPRPAERLTAEVLCHPWIRDHGVAPDRPLDPAVLRLKQFSAMNKL 313  
QY 313 KMAALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSELMESEIKSLM 372  
DB 314 KMAALRVIAESLSEEEIAGLKEMFTWDTNSGAIYDELKEGLKXVGTLDKTEIRDLM 373  
QY 373 DAADIDNSGTTIDYGEFFAATLHMKNKVEREILVAAFDPKDQSGVITIDELQSACTERG 432  
DB 374 DAADIDNSGTTIDYIEFTAAATLHKLREERELHVAAPFDPKQSGVITVDELQACKHN 433  
QY 433 LCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRMTMMKNLNFNIAD 484  
DB 434 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMNSLNISMWD 485

RESULT 7  
T03271  
C/Species: Vigna radiata (mung bean)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-Jun-1999  
C/Accession: S71770  
R:Botella, J.R.; Arteca, J.M.; Somodevilla, M.; Arteca, R.N.  
Plant Mol. Biol. 30, 1129-1137, 1996  
A/Title: Calcium-dependent protein kinase gene expression in response to physical and chemical stress in mung bean.  
A/Reference number: S71770; MUID:96311003; PMID:8704124  
A/Accession: S71770

A/Molecule type: mRNA  
A/Residues: 1-487 <BOT>  
A/Cross-references: EMBL:U08140; NID:G967124; PIDN:AAC49405.1; PID:G967125  
A/Experimental source: strain Rvlicz, cv. Berken, clone pV-CDPK-1  
C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F/22-282/Domain: protein kinase homology <KIN>  
F/30-38/Region: protein kinase ATP-binding motif  
F/325-357/Domain: calmodulin repeat homology <EF2>  
F/361-393/Domain: calmodulin repeat homology <EF3>  
F/397-429/Domain: calmodulin repeat homology <EF4>  
F/431-463/Domain: calmodulin repeat homology <EF5>  
F/53/Active site: Lys #status predicted

Query Match 67.5%; Score 1751; DB 1; Length 487;  
Best Local Similarity 69.1%; Pred. No. 2e-58;  
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;  
QY 14 VLPYQTPRLRDHYLLGKLGOGQFGTTLCTEKSANSYACKSPKRLKVCREDYEDVW 73  
DB 12 VLGHTPNIRDDYTLGRKLGOGQFGTTLCTENSTNEYACKSISKRLISKEDVEDVR 71  
QY 74 REIQMHLSSEHPNVVRIRKGYEDSVFVHVMVECGEGELFDRIVSKGHFSERAVKLIK 133  
DB 72 REIQMHLSGHKNVITIKGAYEDPLVHVMELCAGGELFDRIIQRGHYTERKAAELTKI 131  
QY 134 ILGVVACHSLGWHRDLKPENFLPDSKDDAKLKTATDGLSVFKPGQYLYDVVGSPPY 193  
DB 132 IIVGVVACHSLGWHRDLKPENFLVNRKDDLSUKADFGLSVFFKPGQVTFDVVGSPPY 191  
QY 194 YVAPEVLKCKYGPIDVWSAGVILYLLSGVPPFWAETSGIFRQIQLOGKLDKSDPWPMT 253  
DB 192 YVAPEVLKHYGPADVTAGVILYLLSGVPPFWAETQGGIFDAVLKGHIDFSDPWP 251  
QY 254 SEAAKOLIIYKMLERSPKKRISEAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKI 313  
DB 252 SDSGKOLIRKMLCSQPSERLTAHQVLPCHPWICENGAPDRAIDPAVLRLKQFSAMNKL 311  
QY 314 KMAALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVGSELMESEIKSLM 373  
DB 312 KMAALRVIAESLSEEEIAGLRNFQAVDTNSGAIYDELKAGLRRYGTLDKVEIRDLME 371  
QY 374 DAADIDNSGTTIDYGEFFAATLHMKNKVEREILVAAFDPKDQSGVITIDELQSACTERG 433  
DB 372 AADVXSGTTIDYGEFFAATLHKLREERELHVAAPFDPKQSGVITVDELQOACAEFNM 431  
QY 434 CDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRMTMMKNLNFNIAD 485  
DB 432 TDAFLIEDIIRREVDDNDGRIDYGEFVAMTKGNMGVGR-RTMNSLNISMWD 483

RESULT 8  
T03263  
C/Species: Zea mays (maize)  
C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000  
C/Accession: T03263  
R:Saijo, Y.; Hata, S.; Sheen, J.; Izui, K.  
Biochim. Biophys. Acta 1350, 109-114, 1997  
A/Title: CDNA cloning and prokaryotic expression of a maize calcium-dependent protein kinase  
A/Reference number: Z14815; MUID:97201047; PMID:9048876  
A/Accession: T03263  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-554 <SAI>  
A/Cross-references: EMBL:D87042; NID:G1504051; PIDN:BAAL3232.1; PID:G1504052  
A/Experimental source: strain inbred line H84, clone CDPK7  
C/Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C/Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F/89-343/Domain: protein kinase homology <KIN>  
F/197-105/Region: protein kinase ATP-binding motif  
F/392-424/Domain: calmodulin repeat homology <EF1>  
F/428-460/Domain: calmodulin repeat homology <EF2>

F;464-496/Domain: calmodulin repeat homology <EF3>  
F;498-530/Domain: calmodulin repeat homology <EF4>  
F;120/Active site: Lys #status Predicted

Query Match 67.3%; Score 1745; DB 1; Length 554;  
Best Local Similarity 70.0%; Pred. No. 3.8e-58;  
Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGQFGTTCLCTEKSTSYACKSIPKRLKVCREDYEDVW 72  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 73 REIQIMHLSHPNNVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSERAVKLIK 132  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 197

QY 138 REIQIMHLSGHTNNVAIKGAYEDQLYVHIVMELCAGGELFDRIIQRGHYSERKAAEUTR 197  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 133 TIIGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLYDVVGSPY 192  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 198 IIVGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLYDVVGSPY 257  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 193 YVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDF 245  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 252 YVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDF 245  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 258 YVAPVILKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDF 245  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 253 ISPAKDLIYMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQNNKI 312  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 318 ISPAKDLIYMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQNNKI 312  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 313 KQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLM 372  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 378 KQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLM 372  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 373 DAADINSGTIDYGEFLAATLHNMKREBEILVAAPSDPKDGSVYIIDELOSACTEFG 432  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 438 DAADINSGTIDYGEFLAATLHNMKREBEILVAAPSDPKDGSVYIIDELOSACTEFG 432  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 433 LCDTPDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIADAFG 487  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

QY 498 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMNSLNISMMDAPG 552  
Db SVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLITREDVDVR 137

RESULT 9  
T06126  
calcium-dependent protein kinase (EC 2.7.1.-) CPK5 - Arabidopsis thaliana  
N;Alternate names: protein F23E12.130  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 21-Jan-2000  
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hohnsels, submitted to the Protein Sequence Database, April 1999  
A;Reference number: Z15485  
A;Accession: T06126  
A;Molecule type: DNA  
A;Residues: 1-556 <BEV>  
A;Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.130  
A;Experimental source: cultivar Columbia; BAC clone F23E12  
C;Genetics:  
A;Gene: CPK5; ATSP:F23E12.130  
A;Map position: 4  
A;Introns: 252/1; 300/1; 351/1; 389/3; 445/3; 520/3  
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C;Keywords: EF hand; phosphotransferase; protein kinase  
F;93-355/Domain: protein kinase homology <KIN>  
F;398-430/Domain: calmodulin repeat homology <EF1>  
F;434-466/Domain: calmodulin repeat homology <EF2>  
F;470-502/Domain: calmodulin repeat homology <EF3>  
F;504-536/Domain: calmodulin repeat homology <EF4>

Query Match 67.2%; Score 1742; DB 2; Length 556;  
Best Local Similarity 68.4%; Pred. No. 4.9e-58;  
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;

QY 6 NPRRDSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTCLCTEKSTSYACKSIPKRLKVC 65

Db 77 NPDNQAYVHLGKTPNRIIVTLSRKLGQGGQFGTTCLCTIASVDYACKSISKRLISK 136  
QY 66 EDYEDVMEIREIQIMHLSHPNNVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 125  
Db 137 EDYEDVMEIREIQIMHLSHPNNVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 196  
QY 126 EAVKLIKILGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLY 185  
Db 197 KAAELTKIIVGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLY 256  
QY 186 DVVGSPYVAPSVLKKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDF 245  
Db 257 DVVGSPYVAPSVLKKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKGLDF 316  
QY 246 KSDPPTTSEAAKOLIYKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQ 305  
Db 317 ESDPFPVSDSAKOLIRMLRSKPAERLTAHEVLHRHWCENGVPADRALDPAVLSRLKQ 376  
QY 306 FSOINKIKQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELME 365  
Db 377 FSOINKIKQVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELME 436  
QY 366 SEIKSLMDAADINSGTIDYGEFLAATLHNMKREBEILVAAPSDPKDGSVYIIDELO 425  
Db 437 TEIHDLMDAADINSGTIDYGEFLAATLHNMKREBEILVAAPSDPKDGSVYIIDELO 496  
QY 426 SACTEFGLCDTPDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD 484  
Db 497 QACVERGMADVLEDIIKEVDQNDGKIDYGEFVEMKQGNAGVGR-RTMNSLNISMVD 555  
QY 485 A 485  
Db 556 A 556

RESULT 10  
D84550  
probable calmodulin-domain protein kinase CPK6 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Mar-2001  
C;Accession: D84550  
M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varkken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: D84550  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-544 <STO>  
A;Cross-references: GB:AE002093; NID:G2623752; PIDN:AA86506.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g17290  
A;Map position: 2  
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C;Keywords: EF hand

Query Match 66.8%; Score 1731; DB 2; Length 544;  
Best Local Similarity 68.3%; Pred. No. 1.2e-57;  
Matches 328; Conservative 65; Mismatches 85; Indels 2; Gaps 2;

QY 6 NPRRDSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTCLCTEKSTSYACKSIPKRLKVC 65  
Db 65 NVNQSYVVLGHTPTNLRDLALGRLGKLGQGGQFGTTCLCTELATGVDYACKSISKRLISK 124  
QY 66 EDYEDVMEIREIQIMHLSHPNNVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 125  
Db 125 EDYEDVMEIREIQIMHLSHPNNVRIKGTIEDSVFVHIVMEVCEGGELEFDRIVSKGHFSE 184  
QY 126 EAVKLIKILGVVEACHSLGWHRDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQVLY 185

Db 185 KAALTKIIVGVVEACHSLGVNHRDLKPENFLVNKDDFSLKAIDFGLSVFFKPGQIFK 244  
 QY 186 DVVSGSVYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFROILOGLKDF 245  
 Db 245 DVVSGSVYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFROILOGLKDF 304  
 QY 246 KSPFWPTISEAAKDLIKYKLESPKRSKRSISAEALCHPWIVDEQAAPKPLDPAVLSRLKQ 305  
 Db 305 DTPFWFVSDSADKDLIRKMLCSPPSERLTAHEVLRHPWICENGAVPDRALDPAVLSRLKQ 364  
 QY 306 FSOVNIKKMARLVIAERLSEEEIGGLKELFMIDTNSGTTITPEELKAGLRKRVGSELM 365  
 Db 365 FSAVNIKKMARLVIAERLSEEEIGGLKELFMIDTNSGTTITPEELKAGLRKRVGSELM 424  
 QY 366 SEIKSMDADINDSGTIDYGFPLAATLHMKNVREELVAAFDKDGSGYITIDELQ 425  
 Db 425 TEIRDLEAADVNSGTIDYGFPLAATLHMKNVREELVAAFDKDGSGYITIDELQ 484  
 QY 426 SACTEFLGCDTLPDDMIKIDLDNGDKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD 484  
 Db 485 QSCIEHGMDTVLEDDIIEKVQDNDGRIDYEEFVAMQKGNAGVR-RTMKNLSINISMRD 543  
 RESULT 11  
 A49082  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-Jun-1999  
 C:Accession: A49082  
 R:Harper, J.F.; Binder, B.M.; Sussman, M.R.  
 Biochemistry 32, 3282-3290, 1993  
 A:Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in Esch  
 A:Reference number: A49082; NCBI:128903; NCBI:128904  
 A:Contents: ecotype Columbia  
 A:Accession: A49082  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-610 <HR>  
 A:Cross-references: GB:14771; MID:9289189; PIDN:AAA32761.1; PID:G304105  
 A:Note: sequence extracted from NCBI backbone (NCBI:128903, NCBI:128904)  
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
 F:148-408/Domain: protein kinase homology <KIN>  
 F:156-164/Region: protein kinase ATP-binding motif  
 F:451-483/Domain: calmodulin repeat homology <EF1>  
 F:487-519/Domain: calmodulin repeat homology <EF2>  
 F:523-555/Domain: calmodulin repeat homology <EF3>  
 F:557-589/Domain: calmodulin repeat homology <EF4>  
 F:179/Active site: Lys #status predicted

QY 282 PWIVDEQAAPKPLDPAVLSRLKQFSOMNKKIKMARLVIAERLSEEEIGGLKELFMIDT 341  
 Db 406 PWVQVGVAPDRKPLDSAVLSRMKQFSAMNKKFKMARLVIAERLSEEEIGGLKELFMIDT 465  
 QY 342 DMSGTTITPEELKAGLRKRVGSELMSEELSLMDADINDSGTIDYGEFLAATLHMKNVRE 401  
 Db 466 DKSGQITFELKAGLRKRVGSELMSEELSLMDADINDSGTIDYGEFLAATLHMKNVRE 525  
 QY 402 EILVAFAFDFKDGSGYITIDELQSACTEFLGCDTLPDDMIKIDLDNGDKIDFSEFTAM 461  
 Db 526 DHLFAAFTYFDKDGSGYITIDELQSACTEFLGCDTLPDDMIKIDLDNGDKIDFSEFTAM 585  
 QY 462 MRKGDGVGRSRTMMKNLNFNIAD 483  
 Db 586 MQKSGITGGPVVQGLEKSFSLA 607  
 RESULT 12  
 T09940  
 C:Species: Cucurbita pepo (pumpkin)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
 C:Accession: T09940  
 R:Billard-Ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.  
 Plant Mol. Biol. 39, 199-208, 1999  
 A:Title: Cloning, expression and N-terminal myristoylation of CcCPK1, a calcium-depende  
 A:Reference number: Z16898; MUID:99178773; PMID:10080688  
 A:Accession: T09940  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-573 <ELL>  
 A:Cross-references: EMBL:U90362; NID:91899174; PIDN:AAB49984.1; PID:91899175  
 A:Experimental source: etiolated hypocotyls  
 C:Genetics:  
 A:Gene: CPK1  
 C:Function:  
 A:Description: serine/threonine-specific protein kinase activated by direct binding of  
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki  
 C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotrar  
 F:108-368/Domain: protein kinase homology <KIN>  
 F:447-479/Domain: calmodulin repeat homology <EFH>  
 Query Match 65.9%; Score 1709.5; DB 2; Length 573;  
 Best Local Similarity 64.8%; Pred. No. 8e-57;  
 Matches 321; Conservative 78; Mismatches 79; Indels 17; Gaps 3;  
 QY 4 KNPDR-----RP-----SNTVLPYQTPRLRDHYLLGKLGQGGQFGTTVLCCTEKS 47  
 Db 72 KPPEPMPKVRPYMKRVGSAGLRGGSVLQTKTGNFKYISLGKLGQGGQFGTTVLCVCKA 131  
 QY 48 TSANYACKSIPTKELVCREDEYEDVWREIQIMHHLSEHPNVRIRKTYEDSVFVHIVMEVC 107  
 Db 132 TGKEYACKSIPTKELVCREDEYEDVWREIQIMHHLSEHPNVRIRKTYEDSVFVHIVMEVC 191  
 QY 108 EGGELPRLIVSKGHFEREAVKLIKITLVGVEACHSLGVNHRDLKPENFLDPSKDAKL 167  
 Db 192 AGGELFRIIRQGHYTERKAAELTRIVGVLEACHSLGVNHRDLKPENFLVSKBEBSLL 251  
 QY 168 KATDFGLSVFYKPGQVLYDVVSGSVYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFW 227  
 Db 252 KTIIDFGLSMFEPKPGKFNVDVSGSVYVAPEVLKRYGPEADVMSAGVILYLLSGVPPFW 311  
 QY 228 AETESGIFROILOGLKDFKSDWPPTISEAAKDLIKYKLESPKRSKRSISAEALCHPWIVDE 287  
 Db 312 AESSEGIFEBVLHGDLDFSSDPWPSISDSAKDLVRRMLVRDPRKELTAYELVCHPWVQVD 371  
 QY 288 QAAPKPLDPAVLSRLKQFSOMNKKIKMARLVIAERLSEEEIGGLKELFMIDTNSGTI 347  
 Db 372 GVAFDKELDSAVLTLKQFSAMNKKFKMARLVIAERLSEEEIGGLKELFMIDTNSGTI 431  
 QY 348 TFEELKAGLRKRVGSELMSEELSLMDADINDSGTIDYGEFLAATLHMKNVREELVAA 407



probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Mar-2001  
 C:Accession: H84810  
 R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-769, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: H84810  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-583 <STO>  
 A:Cross-references: GB:AE002093; NID:g3928078; PIDN:AAC79604.1; GSPDB:GM00139  
 C:Genetics:  
 A:Gene: At2g38910  
 A:Map position: 2  
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
 C:Keywords: EF hand

Query Match 63.3%; Score 1640.5; DB 2; Length 583;  
 Best Local Similarity 66.9%; Pred. No. 2.9e-54;  
 Matches 307; Conservative 67; Mismatches 84; Indels 1; Gaps 1;  
 QY 12 NTVLPYQTPRLRDHVLKGLKQGGQGGTTLCTEKTSTANYACKSIPIKRLVCREYEDV 71  
 Db 120 DSVLGRKTENLXDIYSVGRKLGQGGQGGTFLCVDKTKGKEFACKTIKRLTTPDEV 179  
 QY 72 WREIQIMHLSHPNVRIKGYEYDSVFVHVMEVCEGELFDRIVSKGHFSREAVKLI 131  
 Db 180 RREIQIMHLSHPNVRIQVGVAYDAVAVHVMETACAGGELFDRIIORGHYTEKKAELA 239  
 QY 132 KTLIGVVEACHSLGVNHRDLKPENFLFDSPKDDAKIKATDFGLSVFYKPGQYLYDVVWGP 191  
 Db 240 RIIVGVIEACHSLGVNHRDLKPENFLFVSGDEAALKTIDFGLSVFPKPGCTFTDVVWGP 299  
 QY 192 YVVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFROILQKGLDFKSDPWP 251  
 Db 300 YVVAPEVLKRGYSHCECDVWSAGVILYLLSGVPPFWDETEQIGIEQVLKGLDFISEPWP 359  
 QY 252 TISEAARDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNK 311  
 Db 360 SVSESAKDLVRRMLIRDPKRWTTHEVLCHPWVYDGVVALDKPLDSAVLSRLQQFSAMNK 419  
 QY 312 IKWALRVIAERLSEEEIGLKEPKMIDTNSGTITFEELKAGLKXVGSSELMSEIKSL 371  
 Db 420 LKKIAIKVIAESLSEEEIAGLKEPKMIDTNSGHTLEELKGLDRVADLKDSEILGL 479  
 QY 372 MDAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSYITIDELQSACTEF 431  
 Db 480 MQAADIDNSGTIDYGEFLAAMVHLNKKIEKEDHLFTAFSVFDQDGSYITRDELQACKQF 539  
 QY 432 GLCDTPELDMDIKEDLDNDGKIDFSEFTAMMEKGGGVGR 470  
 Db 540 GLADVHLDDILREVDKNDGRIDYSEFVDMN-QDTGFGK 577

Search completed: February 13, 2003, 21:11:31  
 Job time : 39 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2003, 21:06:32 ; Search time 20 Seconds  
(without alignments)  
1026.539 Million cell updates/sec

Title: US-09-848-806-1  
Perfect score: 2593  
Sequence: 1 METKPNRRRSNTVLPYQTP.....KVLNENIADAFGVDGKSD 495

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1944	75.0	508	1	CDPK SOYEN
2	1724	66.5	610	1	CDP1_ARATH
3	1586	61.2	542	1	CDP3_ORYSA
4	1482	57.2	533	1	CDP2_ORYSA
5	1460.5	56.3	513	1	CDP2_WAIZE
6	1460	56.3	534	1	CDP1_ORYSA
7	1432.5	55.2	532	1	CDPK DAUCA
8	854	32.9	602	1	CRK DAUCA
9	591	22.8	499	1	KCCD_HUMAN
10	589.5	22.7	374	1	KCC1_RAT
11	587.5	22.7	370	1	KCC1_HUMAN
12	578.5	22.3	473	1	KCC4_HUMAN
13	574.5	22.2	533	1	KCCD_RAT
14	574	22.1	469	1	KCC4_MOUSE
15	572	22.1	474	1	KCC4_RAT
16	571.5	22.0	542	1	KCCB_MOUSE
17	569.5	22.0	542	1	KCCB_RAT
18	567.5	21.9	478	1	KCCA_HUMAN
19	566.5	21.8	664	1	KCCB_HUMAN
20	563.5	21.7	478	1	KCCA_RAT
21	549.5	21.2	478	1	KCC4_MOUSE
22	544.5	21.0	529	1	KCCG_MOUSE
23	543.5	21.0	472	1	KCCG_HUMAN
24	539	20.8	527	1	KCCG_RAT
25	534.5	20.6	424	1	KPSB_HUMAN
26	533.5	20.6	386	1	KPBG_HUMAN
27	532.5	20.5	386	1	KPBG_RABIT
28	526	20.3	387	1	KPBG_RAT
29	524.5	20.2	387	1	KPBG_MOUSE
30	514.5	19.8	295	1	KMLC_DICDI
31	509	19.6	1431	1	DAPK_HUMAN
32	505	19.5	433	1	DKK1_RAT
33	505	19.5	740	1	DCK1_HUMAN

34	505	19.5	756	1	DCK1_MOUSE
35	499	19.2	335	1	KCC1_SCHPO
36	489.5	18.9	732	1	K6AA_CHICK
37	486	18.7	735	1	K6A1_RAT
38	484.5	18.7	512	1	K110_ARATH
39	482.5	18.6	733	1	K6A2_HUMAN
40	481	18.5	724	1	K6A1_MOUSE
41	480	18.5	735	1	K6A1_HUMAN
42	479	18.5	546	1	CHK2_MOUSE
43	477	18.4	733	1	K6AA_XENLA
44	476.5	18.4	733	1	K6A2_MOUSE
45	476	18.4	543	1	CHK2_HUMAN

ALIGNMENTS

RESULT 1  
CDPK\_SOYEN  
ID CDPK\_SOYEN STANDARD; PRT; 508 AA.  
AC P28583;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calcium-dependent protein kinase SK5 (EC 2.7.1.1-) (CDPK).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Williams;  
RX MEDLINE=91240279; PubMed=1852075;  
RA Harper J.F., Suesman M.R., Schaller G.E., Putnam-Evans C.,  
RA Chatbonneau H., Harmon A.C.;  
RT "A calcium-dependent protein kinase with a regulatory domain similar  
to calmodulin."  
RL Science 252:951-954 (1991)  
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT  
INVOLVE CALCIUM AS A SECOND MESSENGER.  
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY  
PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.  
CC -!- TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.  
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -!- CAMK SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; M64987; AAB00806.1; -.  
PIR; A43713; A43713.  
HSP; Q83450; 1A06.  
InterPro; IPR002048; EF-hand.  
InterPro; IPR000719; Euk\_pkinase.  
InterPro; IPR002290; Ser\_thr\_pkinase.  
Pfam; PF00036; ehand; 4.  
Pfam; PF00069; pkinase; 1.  
ProDom; PD000001; Euk\_pkinase; 1.  
ProDom; PD000012; EF-hand; 2.  
SMART; SM0054; Efh; 4.  
SMART; SM00220; S\_TKC; 1.  
PROSITE; PS00018; EF\_HAND; 4.  
PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.



```
Db 286 HEDSLKTTDFGLSMFFKDDVFTDVVGSPYVAPEVLRKRYGDEADWWSAGVIVYLLS 345
Qy 222 GVPFPWAETESGIFRQILGKLDKDPMTPTISEAAKDLIYKMLERSPKRIISAHEALCH 281
Db 346 GVPFPWAETEQIFRQVLHGLDFSSDWPSTSESAXDLVRKMLVRDPKRLTAHQVLCH 405
Qy 282 PWIVDQRAAPDKPLPAVLRLKQFSQNNKIKQVALRVIAERLSEERIGGKELFKMIDT 341
Db 406 PWQVQGVAPDKPLDPAVLRLKQFSQNNKIKQVALRVIAERLSEERIGGKELFKMIDT 465
Qy 342 DMSGTTTFBELKAGLRKRGVSELMSEIKSLMDAADINDSGTIDYGEFLAATLHMKNQVRE 401
Db 466 DRKSGQITFELKAGLRKRGVSELMSEIKSLMDAADINDSGTIDYGEFLAATLHMKNQVRE 525
Qy 402 EILVAAPSDPKDQSGYITIDELQACTEFGLCDFPLDDMIKEIDLNDGKIDSEBETAM 461
Db 526 DHLFAATFYDKDQSGYITIDELQACTEFGVVEDVRIELMRDQDNDGRIDYNEFVAM 585
Qy 462 MRKGDGVGRSRTMKNLFNIA 483
Db 586 MQKGSITGGPVKXLEKSPSIA 607

RESULT 3
CDP3_ORYSA
ID CDP3_ORYSA STANDARD; PRT; 542 AA.
AC P53684;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 11 (EC 2.7.1.-) (CDPK 11).
GN CPK11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Arborio; TISSUE=coleoptile;
RA MEDLINE=95284352; PubMed=7766885;
RA Breviario D., Morello L., Giani S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
RT calcium-dependent protein kinases.";
RL Plant Mol. Biol. 27:953-967(1995).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
CC THEM SEEM TO BE NON FUNCTIONAL.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
-----
CC EMBL; X81393; CAA57156.1; -
CC HSPSP; Q63450; 1A05
CC InterPro; IPR002048; EF-hand.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00036; ehand; 4.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC ProDom; PD000012; EF-hand; 2.
CC SMART; SM00054; EHF; 3.
CC SMART; SM00220; S_TKC; 1.
```

```
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multi-gene family.
FT DOMAIN 79
FT NP_BIND 81 89 ATP (BY SIMILARITY).
FT BINDING 107 107 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 499 510 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 542 AA; 61166 MW; D4D25275C126DDA CRC64;

Query Match 61.28; Score 1586; DB 1; Length 542;
Best Local Similarity 63.9%; Pred. No. 1.5e-72;
Matches 304; Conservative 68; Mismatches 102; Indels 2; Gaps 2;

Qy 11 SNTVLPTQTPRLRDHYLLGKLGQGGQFGTTLCTEKSANYACKSIPKRLVCRDYEY 70
Db 64 SINVLGRKTADLRSHYIIGRKLGQAQFGTTLCTEINTGCEYACKTIPKRLTKEDVED 123
Qy 71 VVREIQIMHLSHPNPVRIKGYEDSVFHHVNEVCEGSELFDRIIVSKGHFSERBAVL 130
Db 124 VVREIQIMHLSGHNNVVAIKDVEDQAVHIVNELCAGGELFDRIQERGHYSERKAAEL 183
Qy 131 IKTLGVVVEACHSLQVHRDLKPNFLFDSPKDAKATKATDFGLSVFYKPGQYLYDVVGS 190
Db 184 TRIIVSIAMCHSLQVHRDLKPNFLLLDKDDLSIKATDFGLSVFYKPGQVFTLVGS 243
Qy 191 PYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILGKLDKFSDDPW 250
Db 244 PYVAPEVLKRYGPESDVWSAGVILYLLSGVPPFWAETQQGIFDAVLKGHIDFQSDPW 303
Qy 251 PTISAADKDLIVKMLERSPKKRIISAHEALCHPWIVDQAAPDKPLDPAVLRLKQFSQVN 310
Db 304 PAKISADKDLIRKMLSHCPSERLKXAEVLRHPWICENGVAIDQALDPSVLRKQFSQVN 363
Qy 311 KIKKVALRVIAERLSEERIGGKELFKMIDTNSGTTTFBELKAGLRKRGVSELMSEIKS 370
Db 364 KUKLALRVIAERLSEERIGGKELFKMIDTNSGTTTFBELKAGLRKRGVSELMSEIKS 423
Qy 371 LMDAADINDSGTIDYGEFLAATLHMKNQVREIILVAAPSDPKDQSGYITIDELQSACTE 430
Db 424 IMEAHNDNNVTIHYEEFIAATLPLNKIEREHLAAFTYFDKDGSGYIIVDKLQACGE 483
Qy 431 FGLCDTPLDDMIKEIDLNDGKIDSEBETAMMRKGDGVGRS-RTMKNLFNIA 485
Db 484 HNMDLSLLEIISVDQNDQDIDVAEPVAMM-QGSNVLGQWQTMESLNVALLRDA 538

RESULT 4
CDP2_ORYSA
ID CDP2_ORYSA STANDARD; PRT; 533 AA.
AC P53683;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 2 (EC 2.7.1.-) (CDPK 2).
GN CPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Arborio; TISSUE=coleoptile;
RA MEDLINE=95284352; PubMed=7766885;
RA Breviario D., Morello L., Giani S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
RT calcium-dependent protein kinases.";
RL Plant Mol. Biol. 27:953-967(1995).
```

```

RL Plant Mol. Biol. 27:953-967(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR HMBL; X81394; CAA57157.1; -.
DR HSPP; Q63450; IA06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST_1.
DR PROSITE; PS00110; PROTEIN_KINASE_ST_2.
DR PROSITE; PS00111; PROTEIN_KINASE_ST_3.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multiligene family.
KW DOMAIN 85 343
FT NP_BIND 91 99 ATP (BY SIMILARITY).
FT BINDING 114 114 ATP (BY SIMILARITY).
FT ACT_SITE 209 209 BY SIMILARITY.
FT CA_BIND 398 409 EF-HAND 1 (POTENTIAL).
FT CA_BIND 434 445 EF-HAND 2 (POTENTIAL).
FT CA_BIND 470 481 EF-HAND 3 (POTENTIAL).
FT CA_BIND 505 516 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 533 AA; 59522 MW; DOBC570ABD289E28 CRC64;
Query Match 57.2%; Score 1492; DB 1; Length 533;
Best Local Similarity 61.3%; Pred. No. 2.e-98;
Matches 284; Conservative 75; Mismatches 96; Indels 6; Gaps 3;
QY 4 KPNRRPSNTVLPQTPRLRDYHLGKLGQGGQGTIVLCTEKSANYACKSIPKRLV 63
DB 67 KTP-----DTILGKYDDVRSVSLGKELGRGQGVTLCTEIASGKQYACKSISKEKL 122
QY 64 CREYEDVWREIQIMHLSHNPVRIKGTVEDSVFVHIMVCEGEGELFDRIVSKHPS 123
DB 123 SKADKEDIRREIQIMHLSHNPVRIKGTVEDSVFVHIMVCEGEGELFDRIVSKHPS 182
QY 124 EBAVKLIITLIGWEACHSLGVMRDLPENFLDPSKDDAKLKTDFGLSVFYKPGQV 183
DB 183 ERAATICRAVNVNCHFMGMARDLPENFLATKEENAMKATDFGLSVFIKGM 242
QY 184 LYDVGSPPYVAPEVKCYGPEIDVWSAGVILYLLSGVPPFAETSGIFPILOGLK 243
DB 243 YRDIIVGSAVYVAPEVLRNRYKGEIDVWSAGVILYLLSGVPPFAETSGIFPILOGL 302
QY 244 DFKSDWPPTISEAKDLIYKMLERPKRISAEALCHPWTVDQAPDKPLDPAVLSRL 303
DB 303 DFKSDWPPTISEAKDLIYKMLERPKRISAEALCHPWTVDQAPDKPLDPAVLSRL 361
QY 304 KQPSQVKKIKOMALRYIARLSEEEIGGLKELFKWIDTNSGTTTFEELKAGLRKVGSEL 363
DB 362 KQPSQVKKIKOMALRYIARLSEEEIGGLKELFKWIDTNSGTTTFEELKAGLRKVGSEL 421
QY 364 MESEIKSLMDAADINDSGIDYGEFLAALTHNWKVEREILLVAASDFDKDGSVITIDE 423

```

```

Db 422 SAAEVKQLWEADVNGSGIDYVEFITATMRHKLDERDEHLKFAQYFDKNSGFITRDE 481
QY 424 LOSACTGELCDT-PLDDMIKELDNDGKIDFSEFTAMRKG 465
Db 482 LESALIEHEMGDTSTIKDIISEVDFTDNDGRINYEFCAMRGG 524

RESULT 5
CDP2_MAIZE STANDARD; PRT; 513 AA.
ID CDP2_MAIZE
AC P49101;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase 2 (EC 2.7.1.1-) (CDPK 2).
GN CDPK2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Merit; TISSUE=Root tip;
RX MEDLINE=95281563; PubMed=7761420;
RA Patil S.; Takezawa D.; Poovalan B.W.;
RT "Chimeric plant calcium/calmodulin-dependent protein kinase gene with
RT a neural visinin-like calcium-binding domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:4897-4901(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION
CC OF THE KINASE ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; U28376; AAA69507.1; -.
DR HSPP; Q63450; IA06.
DR MaizeDB; 56895; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST_1.
DR PROSITE; PS00110; PROTEIN_KINASE_ST_2.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation.
KW DOMAIN 65 323 PROTEIN_KINASE.
FT NP_BIND 71 79 ATP (BY SIMILARITY).
FT BINDING 94 94 ATP (BY SIMILARITY).
FT ACT_SITE 189 189 BY SIMILARITY.
FT CA_BIND 379 390 EF-HAND 1 (POTENTIAL).
FT CA_BIND 415 426 EF-HAND 2 (POTENTIAL).
FT CA_BIND 451 462 EF-HAND 3 (POTENTIAL).
FT CA_BIND 486 497 EF-HAND 4 (POTENTIAL).

```



CDPK\_DAUCA STANDARD; PRT; 532 AA.  
P28582;  
01-DEC-1992 (Rel. 24, Created)  
01-NOV-1997 (Rel. 35, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).  
Daucus carota (Carrot).  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.  
NCBI\_TaxID=4039;  
[1]  
SEQUENCE FROM N.A.  
Choi J.H.;  
Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
[2]  
SEQUENCE OF 108-532 FROM N.A.  
MEDLINE=92003674; PubMed=1912486;  
Suen K.-L., Choi J.H.;  
"Isolation and sequence analysis of a cDNA clone for a carrot  
calcium-dependent protein kinase: homology to  
calcium/calmodulin-dependent protein kinases and to calmodulin.";  
Plant Mol. Biol. 17:581-590(1991)  
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT  
INVOLVE CALCIUM AS A SECOND MESSENGER.  
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY  
PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC CAMK SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X56599; CAA39936.1; -;  
CC PIR; S17759; S17759.  
CC DR HSSP; Q63450; 1A06.  
CC InterPro; IPR002048; EF-hand.  
CC InterPro; IPR000719; Euk\_pkinase.  
CC InterPro; IPR002290; Ser\_thr\_pkinase.  
CC Pfam; PF00036; ehand; 4;  
CC Pfam; PF00069; pkinase; 1.  
CC ProDom; PD000001; Euk\_pkinase; 1.  
CC ProDom; PD000012; EF-hand; 2.  
CC SMART; SM00054; EFh; 4.  
CC SMART; SM00220; S\_TKC; 1.  
CC SMART; SM00018; EF\_HAND; 4.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
CC PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
CC Calcium-binding; Phosphorylation.  
CC KW  
CC DOMAIN 81 339  
CC FT NP\_BIND 87 95 ATP (BY SIMILARITY).  
CC FT BINDING 110 110 ATP (BY SIMILARITY).  
CC FT ACT\_SITE 205 205 BY SIMILARITY.  
CC FT CA\_BIND 395 406 EF-HAND 1 (POTENTIAL).  
CC FT CA\_BIND 431 442 EF-HAND 2 (POTENTIAL).  
CC FT CA\_BIND 465 476 EF-HAND 3 (POTENTIAL).  
CC FT CA\_BIND 500 511 EF-HAND 4 (POTENTIAL).  
CC SEQUENCE 532 AA; 60065 MW; F03E5F036A0AE348 CRC64;  
Query Match 55.2%; Score 1432.5; DB 1; Length 532;  
Best Local Similarity 59.1%; Pred. No. 6.5e-65;  
Matches 278; Conservative 76; Mismatches 107; Indels 9; Gaps 5;  
QY 2 ETKPN--PR---RP--SNTVLPQYTRLRDHYLLGKLGQGFQGTITLCTKSTISANVACK 55

Db 51 QTGSLKPRQVHRPESNTILGKPPEDIRKVTLLGKELGRQFGCVQYCTENSSGQLYACK 110  
QY 56 STPKKLYCRDYEYDVMWEIOIMHHLSEHPNVVIAIKGYEDSVFVHVMEVCEGELFDR 115  
Db 111 SILKKRLVSKNDKEDIKREIQIQLHLSQPNIVFVKGVFEDRQSVHLVMELCAGGELFDR 170  
QY 116 IVSKGHFSEREAVKLIKILGVWEACHSLGVNHRDLKPNFLFDSPPKDDAKLKATDFGLS 175  
Db 171 IIAQGHYSERAAATCRQIVNVVHVCHPMGVNHRDLKPNFLLSSKDKDAMLKATDFGLS 230  
QY 176 VYKKGQVLYDVVGVSPVYVAVELVKCKVGPEDIVWSAGVLYILLGVPPFWAETESGIF 235  
Db 231 VFIEGKVVNRNVGSAYVVAPELVRSYKEDIWSAGVLYILLGVPPFWAETESGIF 290  
QY 236 RQIQGLDFKSDPPTISEAAKOLYIMLERSPKKISAHEALCHPWIVDEQAAPKPL 295  
Db 291 DAILEGVIDFSESEPFWSNSAKDLVRKMLTQDPRRITSAQVLDHFWMRGEGEASDKPI 350  
QY 296 DPAVLSRLQFQSNKKIKMALRVIAERLSBEEIGGLKELFKMIDTNSGTTITFEELKAG 355  
Db 351 DSAVLSRMKQFAMNKLKQLAKVIAESLSBEEIGGLKSMFANMDTKSGTITFEELKSG 410  
QY 356 LKRVGSELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMEREELVAAFSDFDKOG 415  
Db 411 LARLGSKLSEVEVQQLMDAADVDGNGTIDYLEFITATVHRHKLSEYE--HQAFQYFDKDN 468  
QY 416 SGVITIDEQSACTEFLGLCD-TPLDMMIKEIDLNDGKIDFSETANMRK 464  
Db 469 SGFITDELESAMKEYMGDEATIKDIISEVDSNDGRINVDYDFCAMRR 518  
RESULT 8  
CRK\_DAUCA STANDARD; PRT; 602 AA.  
ID CRK\_DAUCA  
AC P33681;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE CDPK-related protein kinase (EC 2.7.1.-) (PK421).  
GN CCK.  
OS Daucus carota (Carrot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.  
OC NCBI\_TaxID=4039;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Jumarot;  
RX MEDLINE=95367641; PubMed=7640352;  
RA Lindzen E., Choi J.H.;  
RT "A carrot cDNA encoding an atypical protein kinase homologous to  
plant calcium-dependent protein kinases.";  
Plant Mol. Biol. 28:785-797(1995).  
RL -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC CAMK SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. ALL SEEMS  
NON FUNCTIONAL.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X83869; CAA59750.1; -;  
CC HSSP; Q63450; 1A06.  
CC InterPro; IPR002048; EF-hand.  
CC InterPro; IPR000719; Euk\_pkinase.  
CC InterPro; IPR002290; Ser\_thr\_pkinase.  
CC Pfam; PF00069; pkinase; 1.  
CC ProDom; PD000001; Euk\_pkinase; 1.

```

DR SMART; SM00220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
KW Repeat.
FT DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-
D-X.
FT REPEAT 20 26 1.
FT REPEAT 27 33 2.
FT REPEAT 34 40 3.
FT DOMAIN 148 410 PROTEIN KINASE
FT NP_BIND 148 410 ATP (BY SIMILARITY).
FT BINDING 150 180 ATP (BY SIMILARITY).
FT ACT_SITE 276 276 BY SIMILARITY.
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 502 513 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 542 553 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT DOMAIN 574 585 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
FT SEQUENCE 602 AA; 67184 MW; 1D10BF68B37BF447 CRC64;
Query Match 32.9%; Score 854; DB 1; Length 602;
Best Local Similarity 41.2%; Pred. No. 5.1e-36;
Matches 184; Conservative 90; Mismatches 155; Indels 18; Gaps 8;
QY 28 LGKLGQGFSTYLCSTKSTANY-----ACKSIPKRLVCRDVEDVWREIQIMHLS 82
DB 150 VGEVGHGFG--YTRAKPKKGFQGVAVKVIKPAKNTTAIEDVRRVKILRALT 207
QY 83 EHNVVRKIGTSDYSVFVHIVMEVCGGELFDRIVSK-GHFSREAVKLIKILGVFAEC 141
DB 208 GHNNLVQYDAFEDHTNYYVMELCEGGLDRLSRGKYTEDDAKAVMIQILNVAVFC 267
QY 142 HSLGVMRDILKPNFLPDSPKDAKLKATDFGLSVKPGQVLYDVGPSYVAVPEVLKK 201
DB 268 HLQGVVRDILKPNFLPDSPKDAKLSQKALDFGLSDYVVKPDERLNDIVGAYVAVPEVLHR 327
QY 202 CYGPEIDWAGVILYILLSGVPPFWAETESGIFRILQGLKDFKSDPWTISEAAKDLI 261
DB 328 SYSTEADVWIGVTSYLLCGSRFPFWARTESGIFRAVLKANLSFDEPPWVSSEAKDFV 387
QY 262 YKMLRSPKGRISHEALCPHWIVDEQAQPKDPAVLRLKQFSQMKIKMALRVIA 321
DB 388 KRLINKDKPRKMTAAQALCHSWIKNSNDI-KFFLDLILFKMLKVVNRSRSPKKAALRLS 446
QY 322 ERLSEEGIGLKELPFKMDITDNGSTIFFELKAGLRVGSGLM-ESEIKSLMDAADIINS 380
DB 447 KTLIVDELFLYKEQFVILEPTKNGTISLENIKQALNRNSTDAMKDSRVLDLVLNALQY 506
QY 381 GTIDYGFFLAATLHNNKVER-----EELVAAFSDPKDGGSYTIDELQSACTEFLCPT 436
DB 507 RMDFEFBCAALSQVHLEALDRWEQCHARCAYDLFFKDGNGRAIMIBELAS---ELGLGPS 563
QY 437 -PLDDMIKEIDLNDGKIDTSEPTAVM 462
DB 564 IPVRAVLHDWIRHTDGLKSLFLGYVKLL 590
RESULT 9
KCCD HUMAN STANDARD; PRT; 499 AA.
AC Q13557; Q9UCQ9; 499 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC
DE 2.7.1.123) (Cam-kinase II delta chain) (Cam kinase II delta subunit)
DE (CAMK-II delta subunit).
GN CAMK2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN SEQUENCE FROM N.A.
RP TISSUE=Myocardium;
RX MEDLINE=99205154; PubMed=10189359;
RA Hoch B., Meyer R., Hetzer R., Krause E.-G., Karczewski P.;
RT "Identification and expression of delta-isoforms of the
RT multifunctional Ca2+/calmodulin-dependent protein kinase in failing
RT and nonfailing human myocardium.";
RL Circ. Res. 84:713-721(1999).
RN SEQUENCE OF 1-243 FROM N.A.
RP TISSUE=Insulinoma;
RA Rochlitz H., Voigt A., Lankat-Bartgeret B., Goeke B., Helmberg H.,
RA Nauck M.A., Schiemann U., Schatz H., Pfeiffer A.;
RT "Cloning of the human calcium/calmodulin dependent protein kinase II
RT isoforms in human beta cells.";
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 302-417 FROM N.A.
RX MEDLINE=97214619; PubMed=9060999;
RA Tomes R.M., Krystal G.W.;
RT "Identification of novel human tumor cell-specific CaMK-II variants.";
RL Biochim. Biophys. Acta 1355:281-292(1997).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; DELTA 1, DELTA 2 (SHOWN HERE),
CC DELTA 3, DELTA 4, DELTA 8, DELTA 9; ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CARDIAC MUSCLE AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF071569; AAD20442.1; -.
CC EMBL; AJ252239; CAB65123.1; -.
CC EMBL; U50361; AAB16866.1; -.
CC HSSP; Q63450; 1A06.
CC Genew; HGNC:1462; CAMK2D.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S TKC; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
CC Phosphorylation; ATP-binding; Neurone; Alternative splicing.
FT DOMAIN 14 272 PROTEIN KINASE.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT CONFLICT 39 39 G -> E (IN REF. 2).
SQ SEQUENCE 499 AA; 56297 MW; BBEF0B669A883E65 CRC64;
Query Match 22.8%; Score 591; DB 1; Length 499;
Best Local Similarity 37.1%; Pred. No. 5.4e-23;
Matches 142; Conservative 65; Mismatches 144; Indels 32; Gaps 9;
QY 21 RLRDHYLLGKLGQGGFGTTLCTEKSTKSTANYACKSIPKRLVCRDVEDVWREIQIMH 80

```





```

DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002230; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD00001; Euk_pkinase; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR Transferase: Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding.
FT DOMAIN 46 300 PROTEIN KINASE.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT CALMODULIN_BINDING (POTENTIAL).
FT DOMAIN 322 341
SQ SEQUENCE 473 AA; 51925 MW; 8FE51E5612326DC CRC64;

Query Match 22.3%; Score 578.5; DB 1; Length 473;
Best Local Similarity 37.2%; Pred. No. 2.1e-22;
Matches 140; Conservative 65; Mismatches 144; Indels 27; Gaps 10;

QY 22 LRDRHYLLGKLGQCGFTTYLCTEKTSTANYACKSIPKRLKVCREDYEDVWREIQIMHHL 81
DB 42 LSDPFEVESLGRGATSVYRCKQKQKQFYALKVLK-----TVDKKIVRTEIGVLLRL 96

QY 82 SEHPNVVRKGTYSDFVHVHVEVCEGGELFDRIYVSKGHFSREAVKLIKILGWVEAC 141
DB 97 S-HPNITKLEIFETPTETISLVLELVTVGGELFDRIYVSKGHFSREAVKLIKILGWVEAC 155

QY 142 HSLGVMHRLDKPENFLDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPYVVAPEVLKK 201
DB 156 HENGIVHRDLKPELNLATAPDAPLKIADFGLSKIVEHVLNKTVCGTFPGYCAPEILRG 215

QY 202 C-YGPEIDVWSAGVILYLSGVPPFWAET-ESGIFROILOGLKDFKSPDPWTFISBAKD 259
DB 216 CAYGPEIDVWSAGVILYLSGVPPFWAET-ESGIFROILOGLKDFKSPDPWTFISBAKD 275

QY 260 LIYKMLERSPKRISAEALCHPMIVDEQAPDKPLDPAVLSLKQFSQWVKIKMALRV 319
DB 276 LVRLKLVLDPKRRLITFOALQHPWTG-KAANFVHMDTA-QKQLQGFNARKLKAQVAV 333

QY 320 IA-ERL--SEIEIGLKLFLPM-----IPTDNGTITFEE-----LKAGLKRKVGSE 362
DB 334 VASSRLGSSASSHSGIQBSKASRDPSPIDQGNEDMKAIPEGEKIQDGAQAQAVKGAQAE 393

QY 363 LMSEIKSLMDAADI 378
DB 394 LMKVQALEKVGADIN 409

RESULT 13
KCDD RAT
ID KCDD RAT STANDARD; PRT; 533 AA.
AC FT1591;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain (EC
DE 2.7.1.123) (Cam-Kinase II delta chain) (Cam kinase II delta subunit)
DE (CAVK-II delta subunit).
GN CAMK2D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90036861; PubMed=2553697;
RA Tobimatsu T., Fujisawa H.;
RT "Tissue-specific expression of four types of rat calmodulin-dependent
RT protein kinase II mRNAs."
RL J. Biol. Chem. 264:17907-17912 (1989).
DB [2]

SEQUENCE OF 314-533 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Aorta, and Skeletal muscle;
RC MEDLINE=93300844; PubMed=8390994;
RA Schworer C.M., Rothblum L.I., Thekkumkara T.J., Singer H.A.;
RT "Identification of novel isoforms of the delta subunit of
RT Ca2+/calmodulin-dependent protein kinase II. Differential expression
RT in rat brain and aorta."
RL J. Biol. Chem. 268:14443-14449 (1993).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC -!- IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; DELTA 1 (SHOWN HERE), DELTA 2,
CC DELTA 3 AND DELTA 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE
CC BRAIN, DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4
CC IN SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL: J05072; AAA40866.1; -
EMBL: L13406; AAA41479.1; -
EMBL: L13407; AAA41480.1; -
EMBL: L13408; AAA41481.1; -
EMBL: L13409; AAA41482.1; -
EMBL: L13410; AAA41483.1; -
EMBL: L13411; AAA41484.1; -
EMBL: L13412; AAA41485.1; -
EMBL: L13413; AAA41486.1; -
EMBL: L13414; AAA41487.1; -
EMBL: L13415; AAA41488.1; -
EMBL: L13416; AAA41489.1; -
EMBL: L13417; AAA41490.1; -
EMBL: L13418; AAA41491.1; -
EMBL: L13419; AAA41492.1; -
EMBL: L13420; AAA41493.1; -
EMBL: L13421; AAA41494.1; -
EMBL: L13422; AAA41495.1; -
EMBL: L13423; AAA41496.1; -
EMBL: L13424; AAA41497.1; -
EMBL: L13425; AAA41498.1; -
EMBL: L13426; AAA41499.1; -
EMBL: L13427; AAA41500.1; -
EMBL: L13428; AAA41501.1; -
EMBL: L13429; AAA41502.1; -
EMBL: L13430; AAA41503.1; -
EMBL: L13431; AAA41504.1; -
EMBL: L13432; AAA41505.1; -
EMBL: L13433; AAA41506.1; -
EMBL: L13434; AAA41507.1; -
EMBL: L13435; AAA41508.1; -
EMBL: L13436; AAA41509.1; -
EMBL: L13437; AAA41510.1; -
EMBL: L13438; AAA41511.1; -
EMBL: L13439; AAA41512.1; -
EMBL: L13440; AAA41513.1; -
EMBL: L13441; AAA41514.1; -
EMBL: L13442; AAA41515.1; -
EMBL: L13443; AAA41516.1; -
EMBL: L13444; AAA41517.1; -
EMBL: L13445; AAA41518.1; -
EMBL: L13446; AAA41519.1; -
EMBL: L13447; AAA41520.1; -
EMBL: L13448; AAA41521.1; -
EMBL: L13449; AAA41522.1; -
EMBL: L13450; AAA41523.1; -
EMBL: L13451; AAA41524.1; -
EMBL: L13452; AAA41525.1; -
EMBL: L13453; AAA41526.1; -
EMBL: L13454; AAA41527.1; -
EMBL: L13455; AAA41528.1; -
EMBL: L13456; AAA41529.1; -
EMBL: L13457; AAA41530.1; -
EMBL: L13458; AAA41531.1; -
EMBL: L13459; AAA41532.1; -
EMBL: L13460; AAA41533.1; -
EMBL: L13461; AAA41534.1; -
EMBL: L13462; AAA41535.1; -
EMBL: L13463; AAA41536.1; -
EMBL: L13464; AAA41537.1; -
EMBL: L13465; AAA41538.1; -
EMBL: L13466; AAA41539.1; -
EMBL: L13467; AAA41540.1; -
EMBL: L13468; AAA41541.1; -
EMBL: L13469; AAA41542.1; -
EMBL: L13470; AAA41543.1; -
EMBL: L13471; AAA41544.1; -
EMBL: L13472; AAA41545.1; -
EMBL: L13473; AAA41546.1; -
EMBL: L13474; AAA41547.1; -
EMBL: L13475; AAA41548.1; -
EMBL: L13476; AAA41549.1; -
EMBL: L13477; AAA41550.1; -
EMBL: L13478; AAA41551.1; -
EMBL: L13479; AAA41552.1; -
EMBL: L13480; AAA41553.1; -
EMBL: L13481; AAA41554.1; -
EMBL: L13482; AAA41555.1; -
EMBL: L13483; AAA41556.1; -
EMBL: L13484; AAA41557.1; -
EMBL: L13485; AAA41558.1; -
EMBL: L13486; AAA41559.1; -
EMBL: L13487; AAA41560.1; -
EMBL: L13488; AAA41561.1; -
EMBL: L13489; AAA41562.1; -
EMBL: L13490; AAA41563.1; -
EMBL: L13491; AAA41564.1; -
EMBL: L13492; AAA41565.1; -
EMBL: L13493; AAA41566.1; -
EMBL: L13494; AAA41567.1; -
EMBL: L13495; AAA41568.1; -
EMBL: L13496; AAA41569.1; -
EMBL: L13497; AAA41570.1; -
EMBL: L13498; AAA41571.1; -
EMBL: L13499; AAA41572.1; -
EMBL: L13500; AAA41573.1; -
EMBL: L13501; AAA41574.1; -
EMBL: L13502; AAA41575.1; -
EMBL: L13503; AAA41576.1; -
EMBL: L13504; AAA41577.1; -
EMBL: L13505; AAA41578.1; -
EMBL: L13506; AAA41579.1; -
EMBL: L13507; AAA41580.1; -
EMBL: L13508; AAA41581.1; -
EMBL: L13509; AAA41582.1; -
EMBL: L13510; AAA41583.1; -
EMBL: L13511; AAA41584.1; -
EMBL: L13512; AAA41585.1; -
EMBL: L13513; AAA41586.1; -
EMBL: L13514; AAA41587.1; -
EMBL: L13515; AAA41588.1; -
EMBL: L13516; AAA41589.1; -
EMBL: L13517; AAA41590.1; -
EMBL: L13518; AAA41591.1; -
EMBL: L13519; AAA41592.1; -
EMBL: L13520; AAA41593.1; -
EMBL: L13521; AAA41594.1; -
EMBL: L13522; AAA41595.1; -
EMBL: L13523; AAA41596.1; -
EMBL: L13524; AAA41597.1; -
EMBL: L13525; AAA41598.1; -
EMBL: L13526; AAA41599.1; -
EMBL: L13527; AAA41600.1; -
EMBL: L13528; AAA41601.1; -
EMBL: L13529; AAA41602.1; -
EMBL: L13530; AAA41603.1; -
EMBL: L13531; AAA41604.1; -
EMBL: L13532; AAA41605.1; -
EMBL: L13533; AAA41606.1; -
EMBL: L13534; AAA41607.1; -
EMBL: L13535; AAA41608.1; -
EMBL: L13536; AAA41609.1; -
EMBL: L13537; AAA41610.1; -
EMBL: L13538; AAA41611.1; -
EMBL: L13539; AAA41612.1; -
EMBL: L13540; AAA41613.1; -
EMBL: L13541; AAA41614.1; -
EMBL: L13542; AAA41615.1; -
EMBL: L13543; AAA41616.1; -
EMBL: L13544; AAA41617.1; -
EMBL: L13545; AAA41618.1; -
EMBL: L13546; AAA41619.1; -
EMBL: L13547; AAA41620.1; -
EMBL: L13548; AAA41621.1; -
EMBL: L13549; AAA41622.1; -
EMBL: L13550; AAA41623.1; -
EMBL: L13551; AAA41624.1; -
EMBL: L13552; AAA41625.1; -
EMBL: L13553; AAA41626.1; -
EMBL: L13554; AAA41627.1; -
EMBL: L13555; AAA41628.1; -
EMBL: L13556; AAA41629.1; -
EMBL: L13557; AAA41630.1; -
EMBL: L13558; AAA41631.1; -
EMBL: L13559; AAA41632.1; -
EMBL: L13560; AAA41633.1; -
EMBL: L13561; AAA41634.1; -
EMBL: L13562; AAA41635.1; -
EMBL: L13563; AAA41636.1; -
EMBL: L13564; AAA41637.1; -
EMBL: L13565; AAA41638.1; -
EMBL: L13566; AAA41639.1; -
EMBL: L13567; AAA41640.1; -
EMBL: L13568; AAA41641.1; -
EMBL: L13569; AAA41642.1; -
EMBL: L13570; AAA41643.1; -
EMBL: L13571; AAA41644.1; -
EMBL: L13572; AAA41645.1; -
EMBL: L13573; AAA41646.1; -
EMBL: L13574; AAA41647.1; -
EMBL: L13575; AAA41648.1; -
EMBL: L13576; AAA41649.1; -
EMBL: L13577; AAA41650.1; -
EMBL: L13578; AAA41651.1; -
EMBL: L13579; AAA41652.1; -
EMBL: L13580; AAA41653.1; -
EMBL: L13581; AAA41654.1; -
EMBL: L13582; AAA41655.1; -
EMBL: L13583; AAA41656.1; -
EMBL: L13584; AAA41657.1; -
EMBL: L13585; AAA41658.1; -
EMBL: L13586; AAA41659.1; -
EMBL: L13587; AAA41660.1; -
EMBL: L13588; AAA41661.1; -
EMBL: L13589; AAA41662.1; -
EMBL: L13590; AAA41663.1; -
EMBL: L13591; AAA41664.1; -
EMBL: L13592; AAA41665.1; -
EMBL: L13593; AAA41666.1; -
EMBL: L13594; AAA41667.1; -
EMBL: L13595; AAA41668.1; -
EMBL: L13596; AAA41669.1; -
EMBL: L13597; AAA41670.1; -
EMBL: L13598; AAA41671.1; -
EMBL: L13599; AAA41672.1; -
EMBL: L13600; AAA41673.1; -
EMBL: L13601; AAA41674.1; -
EMBL: L13602; AAA41675.1; -
EMBL: L13603; AAA41676.1; -
EMBL: L13604; AAA41677.1; -
EMBL: L13605; AAA41678.1; -
EMBL: L13606; AAA41679.1; -
EMBL: L13607; AAA41680.1; -
EMBL: L13608; AAA41681.1; -
EMBL: L13609; AAA41682.1; -
EMBL: L13610; AAA41683.1; -
EMBL: L13611; AAA41684.1; -
EMBL: L13612; AAA41685.1; -
EMBL: L13613; AAA41686.1; -
EMBL: L13614; AAA41687.1; -
EMBL: L13615; AAA41688.1; -
EMBL: L13616; AAA41689.1; -
EMBL: L13617; AAA41690.1; -
EMBL: L13618; AAA41691.1; -
EMBL: L13619; AAA41692.1; -
EMBL: L13620; AAA41693.1; -
EMBL: L13621; AAA41694.1; -
EMBL: L13622; AAA41695.1; -
EMBL: L13623; AAA41696.1; -
EMBL: L13624; AAA41697.1; -
EMBL: L13625; AAA41698.1; -
EMBL: L13626; AAA41699.1; -
EMBL: L13627; AAA41700.1; -
EMBL: L13628; AAA41701.1; -
EMBL: L13629; AAA41702.1; -
EMBL: L13630; AAA41703.1; -
EMBL: L13631; AAA41704.1; -
EMBL: L13632; AAA41705.1; -
EMBL: L13633; AAA41706.1; -
EMBL: L13634; AAA41707.1; -
EMBL: L13635; AAA41708.1; -
EMBL: L13636; AAA41709.1; -
EMBL: L13637; AAA41710.1; -
EMBL: L13638; AAA41711.1; -
EMBL: L13639; AAA41712.1; -
EMBL: L13640; AAA41713.1; -
EMBL: L13641; AAA41714.1; -
EMBL: L13642; AAA41715.1; -
EMBL: L13643; AAA41716.1; -
EMBL: L13644; AAA41717.1; -
EMBL: L13645; AAA41718.1; -
EMBL: L13646; AAA41719.1; -
EMBL: L13647; AAA41720.1; -
EMBL: L13648; AAA41721.1; -
EMBL: L13649; AAA41722.1; -
EMBL: L13650; AAA41723.1; -
EMBL: L13651; AAA41724.1; -
EMBL: L13652; AAA41725.1; -
EMBL: L13653; AAA41726.1; -
EMBL: L13654; AAA41727.1; -
EMBL: L13655; AAA41728.1; -
EMBL: L13656; AAA41729.1; -
EMBL: L13657; AAA41730.1; -
EMBL: L13658; AAA41731.1; -
EMBL: L13659; AAA41732.1; -
EMBL: L13660; AAA41733.1; -
EMBL: L13661; AAA41734.1; -
EMBL: L13662; AAA41735.1; -
EMBL: L13663; AAA41736.1; -
EMBL: L13664; AAA41737.1; -
EMBL: L13665; AAA41738.1; -
EMBL: L13666; AAA41739.1; -
EMBL: L13667; AAA41740.1; -
EMBL: L13668; AAA41741.1; -
EMBL: L13669; AAA41742.1; -
EMBL: L13670; AAA41743.1; -
EMBL: L13671; AAA41744.1; -
EMBL: L13672; AAA41745.1; -
EMBL: L13673; AAA41746.1; -
EMBL: L13674; AAA41747.1; -
EMBL: L13675; AAA41748.1; -
EMBL: L13676; AAA41749.1; -
EMBL: L13677; AAA41750.1; -
EMBL: L13678; AAA41751.1; -
EMBL: L13679; AAA41752.1; -
EMBL: L13680; AAA41753.1; -
EMBL: L13681; AAA41754.1; -
EMBL: L13682; AAA41755.1; -
EMBL: L13683; AAA41756.1; -
EMBL: L13684; AAA41757.1; -
EMBL: L13685; AAA41758.1; -
EMBL: L13686; AAA41759.1; -
EMBL: L13687; AAA41760.1; -
EMBL: L13688; AAA41761.1; -
EMBL: L13689; AAA41762.1; -
EMBL: L13690; AAA41763.1; -
EMBL: L13691; AAA41764.1; -
EMBL: L13692; AAA41765.1; -
EMBL: L13693; AAA41766.1; -
EMBL: L13694; AAA41767.1; -
EMBL: L13695; AAA41768.1; -
EMBL: L13696; AAA41769.1; -
EMBL: L13697; AAA41770.1; -
EMBL: L13698; AAA41771.1; -
EMBL: L13699; AAA41772.1; -
EMBL: L13700; AAA41773.1; -
EMBL: L13701; AAA41774.1; -
EMBL: L13702; AAA41775.1; -
EMBL: L13703; AAA41776.1; -
EMBL: L13704; AAA41777.1; -
EMBL: L13705; AAA41778.1; -
EMBL: L13706; AAA41779.1; -
EMBL: L13707; AAA41780.1; -
EMBL: L13708; AAA41781.1; -
EMBL: L13709; AAA41782.1; -
EMBL: L13710; AAA41783.1; -
EMBL: L13711; AAA41784.1; -
EMBL: L13712; AAA41785.1; -
EMBL: L13713; AAA41786.1; -
EMBL: L13714; AAA41787.1; -
EMBL: L13715; AAA41788.1; -
EMBL: L13716; AAA41789.1; -
EMBL: L13717; AAA41790.1; -
EMBL: L13718; AAA41791.1; -
EMBL: L13719; AAA41792.1; -
EMBL: L13720; AAA41793.1; -
EMBL: L13721; AAA41794.1; -
EMBL: L13722; AAA41795.1; -
EMBL: L13723; AAA41796.1; -
EMBL: L13724; AAA41797.1; -
EMBL: L13725; AAA41798.1; -
EMBL: L13726; AAA41799.1; -
EMBL: L13727; AAA41800.1; -
EMBL: L13728; AAA41801.1; -
EMBL: L13729; AAA41802.1; -
EMBL: L13730; AAA41803.1; -
EMBL: L13731; AAA41804.1; -
EMBL: L13732; AAA41805.1; -
EMBL: L13733; AAA41806.1; -
EMBL: L13734; AAA41807.1; -
EMBL: L13735; AAA41808.1; -
EMBL: L13736; AAA41809.1; -
EMBL: L13737; AAA41810.1; -
EMBL: L13738; AAA41811.1; -
EMBL: L13739; AAA41812.1; -
EMBL: L13740; AAA41813.1; -
EMBL: L13741; AAA41814.1; -
EMBL: L13742; AAA41815.1; -
EMBL: L13743; AAA41816.1; -
EMBL: L13744; AAA41817.1; -
EMBL: L13745; AAA41818.1; -
EMBL: L13746; AAA41819.1; -
EMBL: L13747; AAA41820.1; -
EMBL: L13748; AAA41821.1; -
EMBL: L13749; AAA41822.1; -
EMBL: L13750; AAA41823.1; -
EMBL: L13751; AAA41824.1; -
EMBL: L13752; AAA41825.1; -
EMBL: L13753; AAA41826.1; -
EMBL: L13754; AAA41827.1; -
EMBL: L13755; AAA41828.1; -
EMBL: L13756; AAA41829.1; -
EMBL: L13757; AAA41830.1; -
EMBL: L13758; AAA41831.1; -
EMBL: L13759; AAA41832.1; -
EMBL: L13760; AAA41833.1; -
EMBL: L13761; AAA41834.1; -
EMBL: L13762; AAA41835.1; -
EMBL: L13763; AAA41836.1; -
EMBL: L13764; AAA41837.1; -
EMBL: L13765; AAA41838.1; -
EMBL: L13766; AAA41839.1; -
EMBL: L13767; AAA41840.1; -
EMBL: L13768; AAA41841.1; -
EMBL: L13769; AAA41842.1; -
EMBL: L13770; AAA41843.1; -
EMBL: L13771; AAA41844.1; -
EMBL: L13772; AAA41845.1; -
EMBL: L13773; AAA41846.1; -
EMBL: L13774; AAA41847.1; -
EMBL: L13775; AAA41848.1; -
EMBL: L13776; AAA41849.1; -
EMBL: L13777; AAA41850.1; -
EMBL: L13778; AAA41851.1; -
EMBL: L13779; AAA41852.1; -
EMBL: L13780; AAA41853.1; -
EMBL: L13781; AAA41854.1; -
EMBL: L13782; AAA41855.1; -
EMBL: L13783; AAA41856.1; -
EMBL: L13784; AAA41857.1; -
EMBL: L13785; AAA41858.1; -
EMBL: L13786; AAA41859.1; -
EMBL: L13787; AAA41860.1; -
EMBL: L13788; AAA41861.1; -
EMBL: L13789; AAA41862.1; -
EMBL: L13790; AAA41863.1; -
EMBL: L13791; AAA41864.1; -
EMBL: L13792; AAA41865.1; -
EMBL: L13793; AAA41866.1; -
EMBL: L13794; AAA41867.1; -
EMBL: L13795; AAA41868.1; -
EMBL: L13796; AAA41869.1; -
EMBL: L13797; AAA41870.1; -
EMBL: L13798; AAA41871.1; -
EMBL: L13799; AAA41872.1; -
EMBL: L13800; AAA41873.1; -
EMBL: L13801; AAA41874.1; -
EMBL: L13802; AAA41875.1; -
EMBL: L13803; AAA41876.1; -
EMBL: L13804; AAA41877.1; -
EMBL: L13805; AAA41878.1; -
EMBL: L13806; AAA41879.1; -
EMBL: L13807; AAA41880.1; -
EMBL: L13808; AAA41881.1; -
EMBL: L13809; AAA41882.1; -
EMBL: L13810; AAA41883.1; -
EMBL: L13811; AAA41884.1; -
EMBL: L13812; AAA41885.1; -
EMBL: L13813; AAA41886.1; -
EMBL: L13814; AAA41887.1; -
EMBL: L13815; AAA41888.1; -
EMBL: L13816; AAA41889.1; -
EMBL: L13817; AAA41890.1; -
EMBL: L13818; AAA41891.1; -
EMBL: L13819; AAA41892.1; -
EMBL: L13820; AAA41893.1; -
EMBL: L13821; AAA41894.1; -
EMBL: L13822; AAA41895.1; -
EMBL: L13823; AAA41896.1; -
EMBL: L13824; AAA41897.1; -
EMBL: L13825; AAA41898.1; -
EMBL: L13826; AAA41899.1; -
EMBL: L13827; AAA41900.1; -
EMBL: L13828; AAA41901.1; -
EMBL: L13829; AAA41902.1; -
EMBL: L13830; AAA41903.1; -
EMBL: L13831; AAA41904.1; -
EMBL: L13832; AAA41905.1; -
EMBL: L13833; AAA41906.1; -
EMBL: L13834; AAA41907.1; -
EMBL: L13835; AAA41908.1; -
EMBL: L13836; AAA41909.1; -
EMBL: L13837; AAA41910.1; -
EMBL: L13838; AAA41911.1; -
EMBL: L13839; AAA41912.1; -
EMBL: L13840; AAA41913.1; -
EMBL: L13841; AAA41914.1; -
EMBL: L13842; AAA41915.1; -
EMBL: L13843; AAA41916.1; -
EMBL: L13844; AAA41917.1; -
EMBL: L13845; AAA41918.1; -
EMBL: L13846; AAA41919.1; -
EMBL: L13847; AAA41920.1; -
EMBL: L13848; AAA41921.1; -
EMBL: L13849; AAA41922.1; -
EMBL: L13850; AAA41923.1; -
EMBL: L13851; AAA41924.1; -
EMBL: L13852; AAA41925.1; -
EMBL: L13853; AAA41926.1; -
EMBL: L13854; AAA41927.1; -
EMBL: L13855; AAA41928.1; -
EMBL: L13856; AAA41929.1; -
EMBL: L13857; AAA41930.1; -
EMBL: L13858; AAA41931.1; -
EMBL: L13859; AAA41932.1; -
EMBL: L13860; AAA41933.1; -
EMBL: L13861; AAA41934.1; -
EMBL: L13862; AAA41935.1; -
EMBL: L13863; AAA41936.1; -
EMBL: L13864; AAA41937.1; -
EMBL: L13865; AAA41938.1; -
EMBL: L13866; AAA41939.1; -
EMBL: L13867; AAA41940.1; -
EMBL: L13868; AAA41941.1; -
EMBL: L13869; AAA41942.1; -
EMBL: L13870; AAA41943.1; -
EMBL: L13871; AAA41944.1; -
EMBL: L13872; AAA41945.1; -
EMBL: L13873; AAA41946.1; -
EMBL: L13874; AAA41947.1; -
EMBL: L13875; AAA41948.1; -
EMBL: L13876; AAA41949.1; -
EMBL: L13877; AAA41950.1; -
EMBL: L13878; AAA41951.1; -
EMBL: L13879; AAA41952.1; -
EMBL: L13880; AAA41953.1; -
EMBL: L13881; AAA41954.1; -
EMBL: L13882; AAA41955.1; -
EMBL: L13883; AAA41956.1; -
EMBL: L13884; AAA41957.1; -
EMBL: L13885; AAA41958.1; -
EMBL: L13886; AAA41959.1; -
EMBL: L13887; AAA41960.1; -
EMBL: L13888; AAA41961.1; -
EMBL: L13889; AAA41962.1; -
EMBL: L13890; AAA41963.1; -
EMBL: L13891; AAA41964.1; -
EMBL: L13892; AAA41965.1; -
EMBL: L13893; AAA41966.1; -
EMBL: L13894; AAA41967.1; -
EMBL: L13895; AAA41968.1; -
EMBL: L13896; AAA41969.1; -
EMBL: L13897; AAA41970
```

QY 200 KK-CYCPEIDWAGVILYLLSGVPPWPAETSGIFRQILQKLDKSPWPTTISEAAK 258  
 DB 187 RNDPKYKPVDMWACGVILYLLSGVPPWDEQRLVQKIKAGAYDFPSEWTVIPEAK 246  
 QY 259 DLIYKXLESPKRIISAHEALCHPWVDEQAPDKPLDPAVLSELKQFSQWNIKKWALR 318  
 DB 247 DLINKVLTINPAKRITASEALGHPWCQSTVASMHHQETVDCLEKFNARRKLKG---A 303  
 QY 319 VIAERLSEEEIGLKELFQWID 340  
 DB 304 ILTTLATRNFAAKSLKXPD 325

RESULT 14  
 KCC4 MOUSE STANDARD; PRT; 469 AA.  
 AC P08414; Q61381;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain  
 DE (EC 2.7.1.123) (CAM Kinase-GR) (CaMK IV).  
 GN CAMK4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=91372388; PubMed=1933997;  
 RA Jones D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;  
 RT "cDNA sequence and differential expression of the mouse  
 RT Ca2+/calmodulin-dependent protein kinase IV gene."  
 RL FEBS Lett. 289:105-109(1991).  
 RN [2]  
 RP SEQUENCE OF 240-469 FROM N.A.  
 RX MEDLINE=89122027; PubMed=2536634;  
 RA Sikela J.M., Law M.L., Kao F.-T., Hartz J.A., Wei Q., Hahn W.E.;  
 RT "Chromosomal localization of the human gene for brain  
 RT Ca2+/calmodulin-dependent protein kinase type IV."  
 RL Genomics 4:21-27(1989).  
 RN [3]  
 RP SEQUENCE OF 315-469 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=87204263; PubMed=3033675;  
 RA Sikela J.M., Hahn W.E.;  
 RT "Screening an expression library with a ligand probe: isolation and  
 RT sequence of a cDNA corresponding to a brain calmodulin-binding  
 RT protein."  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042(1987).  
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.  
 CC -1- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL  
 CC NUCLEI.  
 CC -1- TISSUE SPECIFICITY: BRAIN AND TESTIS.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CAMK SUBFAMILY.

-----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL; M16206; AAA39933.1; --  
 EMBL; M64266; AAA37364.1; --  
 EMBL; J03057; AAA37366.1; --  
 EMBL; X58995; CAA41741.1; --  
 PIR; A29878; A29878.  
 PIR; S17656; S17656.

DR HSP; Q63450; 1A06.  
 DR MGD; MGI:88258; Camk4.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SMO0200; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Calmodulin-binding.  
 FT DOMAIN 42 296 PROTEIN KINASE.  
 FT NP\_BIND 48 56 ATP (BY SIMILARITY).  
 FT BINDING 71 71 ATP (BY SIMILARITY).  
 FT ACT\_SITE 160 160 BY SIMILARITY.  
 FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).  
 FT CONFLICT 278 280 VLD -> CFGI (IN REF. 2).  
 FT CONFLICT 302 302 N -> T (IN REF. 2).  
 SQ SEQUENCE 469 AA; 52627 MW; CE1F98670822F975 CRC64;  
 Query Match 22.1%; Score 574; DB 1; Length 469;  
 Best Local Similarity 33.4%; Pred. No. 3.8e-22;  
 Matches 146; Conservative 79; Mismatches 170; Indels 42; Gaps 12;  
 QY 22 LRHYLLGKLGQGFQGTLYLCTEKSTSANVACKSIKPKLVCRDVEDYVMEIQLMHL 81  
 DB 36 LGDFEVESELGRGATSIYRCKQKQKQKPYALVAKK-----TVDKKIVRTIGVLLRL 92  
 QY 82 SEHPNVIRIKGTYESVFVHIVMEVCEGGELFDRIYKSGHFSEREAVKLITLGVVEAC 141  
 DB 93 S-HPNIIKILKEITETPTTEISLVLELVGTGELFDRIYKSGYSEKDARDVAKQILEAVYL 151  
 QY 142 HSLGVHRLDKPENLFDSPKDDAKLKATDFGLSVFVKPGQYLDYVGVSPYVVAPEVLKK 201  
 DB 152 HENGLVHRLDKPENLLYATPADPLKTDGSLKIVHQLVMTVCGTFCYCAPEILRG 211  
 QY 202 C-YGPEIDVMSAGVILYLLSGVPPWPAET-ESGIFRQILQKLDKSPWPTTISEAAK 259  
 DB 212 CAYGPEVDWMSVGIITILLGCFEPFYDERGDFQFMFRILNCEYFFISPMWDEVSLNAK 271  
 QY 260 LIYKMLERSPKRIISAHEALCHPWVDEQAPDKPLDPAVLSELKQFSQWNIKKWALRV 319  
 DB 272 LVKGLVLDPKRRLTFQALQHPWVIG-KAANFVHMDTA-QKLOEFNARKKLAAKAV 329  
 QY 320 IABRLSEEBIGGLKELFKMIDTD---NSGTITFEELKAGLRVGSSELMSEIKSLMDAAD 376  
 DB 330 VA-----SSRLGSASSHTSIQENHKASSDPPSTQAKDSTLLGKKMQEEDQBE----- 379  
 QY 377 IDNSGIDYGEFLAATLHNKMKEREILVAAFSDFKDQSGVITIDELQSACTEFGLCDT 436  
 DB 380 -----DQVEAERSADEMRKQSEEV-----EKDAG--VKEETSSMVPQDPEDL 422  
 QY 437 PLDDMIKEIDLNDGKI 453  
 DB 423 ETDD--PEMKRUSEEKL 437

RESULT 15  
 KCC4 RAT STANDARD; PRT; 474 AA.  
 AC P13234;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain  
 DE (EC 2.7.1.123) (CAM Kinase-GR) (CaMK IV) (Calipermin).  
 GN CAMK4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.  
 RX MEDLINE=91289548; PubMed=1648230;  
 RA Ohmsted C.-A., Bland M.M., Werrill B.M., Sahyoun N.;  
 RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein  
 kinase Gr and caldesmon: a gene within a gene.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=91304387; PubMed=1649385;  
 RA Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,  
 RA Slaughter G.R., Ono T.;  
 RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ  
 cell-specific calmodulin-binding protein are derived from the same  
 gene.";   
 RL Mol. Cell. Biol. 11:3960-3971 (1991).  
 RN [3]  
 RP SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).  
 RX STRAIN=Sprague-Dawley; Tissue=Brain;  
 RC MEDLINE=89174647; PubMed=2538431;  
 RA Ohmsted C.-A., Jensen K.F., Sahyoun N.;  
 RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar  
 granule cells. Identification of a novel neuronal  
 calmodulin-dependent protein kinase.";   
 RL J. Biol. Chem. 264:5866-5875 (1989).  
 RN [4]  
 RP SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361.  
 RX STRAIN=Sprague-Dawley;  
 RC MEDLINE=89123272; PubMed=2914893;  
 RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;  
 RT "Molecular cloning sequence and distribution of rat caldesmon, a  
 high affinity calmodulin-binding protein.";   
 RL J. Biol. Chem. 264:2081-2087 (1989).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=96094352; PubMed=7493991;  
 RA Sun Z., Means R.L., Lemagueresse B., Means A.R.;  
 RT "Organization and analysis of the complete rat calmodulin-dependent  
 protein kinase IV gene.";   
 RL J. Biol. Chem. 270:23507-23514 (1995).  
 CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,  
 ENRICHED IN CEREELLAR GRANULE CELLS.  
 CC -1- FUNCTION: CALDESMON IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING  
 PROTEIN.  
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1/calcium-calmodulin-dependent  
 protein kinase type IV catalytic chain (shown here) and  
 2/caldesmon; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2  
 is testis-specific.  
 CC -1- PTM: THE N-TERMINAL OF CALDESMON IS BLOCKED.  
 CC -1- MISCELLANEOUS: The presence of an alternative promoter gives rise  
 to the testis-specific isoform 2/caldesmon protein.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CAMK SUBFAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR ENBL; M63334; AAA40865.1; -;  
 DR ENBL; M74488; AAA40845.1; ALT\_SEQ.  
 DR ENBL; M64757; AAA40856.1; -;  
 DR ENBL; M64757; AAA40857.1; -;  
 DR ENBL; J04600; AAA41867.1; -;  
 DR ENBL; J04446; AAA40990.1; -;  
 DR PIR; A41103; TVRTC4.  
 DR HSP; Q63450; 1A06  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.

PFam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW transferase, Serine/threonine-protein kinase, ATP-binding,  
 calmodulin-binding, Testis; Alternative splicing.  
 FT DOMAIN 42 296 PROTEIN KINASE.  
 FT NP\_BIND 48 56 ATP (BY SIMILARITY).  
 FT BINDING 71 71 FT (BY SIMILARITY).  
 FT ACT\_SITE 160 160 BY SIMILARITY.  
 FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).  
 FT DOMAIN 333 393 POLY-GLU.  
 FT DOMAIN 403 413 POLY-GLU.  
 FT VARSPLIC 1 305 MISSING (IN ISOFORM 2).  
 FT CONFLICT 372 372 I -> M (IN REF. 2 AND 4).  
 SQ SEQUENCE 474 AA; 53133 MW; 56F71AC5644DED23 CRC64;  
 Query Match 22.1%; Score 572; DB 1; Length 474;  
 Best Local Similarity 34.1%; Pred. No. 4.5e-22;  
 Matches 142; Conservative 75; Mismatches 158; Indels 42; Gaps 11;  
 QY 3 TKEN-PRRSNTVLPYQPRLRDHYLVKK-----LGQGPQTTLCTEKST 48  
 DB 5 TVPSCSPSCSVTSTENLVPDYWDGSKRDLPSDFEVESELGRGATSVYRCKQGT 64  
 QY 49 SANYACKSIPKRLKVCREDYEDVWREIOMHSLSEHPNVRIKGTIYEDSVFVHIVMEVCE 108  
 DB 65 OKPYALKVLKK-----TVDKKIVRTTEIGVLLRLS-HPNIIKLKEIFETPTTEISLVLELVT 118  
 QY 109 GGELFDRIVSKGHFSEREAVKILITLGVACHSLGVMMHDLKPEFLFDSPKDDAKLK 168  
 DB 119 GGELFDRIVEKGYISERDAADAVKQILEAVAYLHENGIVHRLKPELNYLTFAPDAPLK 178  
 QY 169 ATDFGLSVFYKQCYLYDVVGSPPYVAPEVLKCC-YGPEIDVMSAGVILYLILSGVPFFW 227  
 DB 179 IADFGLSKIVEHQVLMKTVCGTPGYCAPILLRGCAYGFEVDMWSVGIIITILLCGPEFFY 238  
 QY 228 AET-ESGIFRQILQGLDFKSPDWTIISAAKDLIYKMLERSPKRISAHEALCHPMIVD 286  
 DB 239 DERGDQFMFERILNCYYFISPMWDEVSNAKDLVKKLIVLDPKKRLTTFQALQHPWVTG 298  
 QY 287 EQAAPDKPLDPAVLRLKQFSQNNKIKKMLRVIAERLSEEEIIGLKELFKMIDTNSGT 346  
 DB 299 -KAANFVHMDTA-QKXLFENARRKKAQVAVVA---SSRLGSASSSHNTICESNKAS 352  
 QY 347 ITFEELKAGLKRVGSELMSEIKSLMDAADINDSGTIDYGEFLAATLHMKNKEREHI 403  
 DB 353 SRAQPAQDGKDK--TDPLENKIOA-----GDHEAAKAAADETKKLOSEEV 395

Search completed: February 13, 2003, 21:12:06  
 Job time : 21 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

XM protein - protein search, using sw model

Run on: February 13, 2003, 20:59:17 ; Search time 74 seconds

(without alignments)  
1378.288 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPSTNVLPLYQTP.....KVLNFIADAFGVDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 21:\*
- 1: sp\_archea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organalle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_proteat:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_virus:\*
  - 16: sp\_bacteriaph:\*
  - 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	10	Q39016 arabidopsis
2	2577	99.4	495	10	Q949P0 arabidopsis
3	2536	97.8	557	10	Q9LQH7 arabidopsis
4	2458	94.8	501	10	Q38869 arabidopsis
5	2030	78.3	490	10	Q24430 glycine max
6	1969.5	76.0	496	10	Q3X19 solanum tub
7	1844.5	71.1	490	10	Q42396 arabidopsis
8	1773	68.4	551	10	Q9FXQ3 oryza sativ
9	1752	67.6	482	10	Q04417 oryza sativ
10	1751	67.5	487	10	Q43676 phaseolus a
11	1745	67.3	554	10	Q04123 oryza sativ
12	1742	67.2	556	10	Q38871 arabidopsis
13	1739.5	67.1	578	10	Q93XJ0 solanum tub
14	1733.5	66.9	578	10	Q3YF3 nicotiana t
15	1731	66.8	544	10	Q38872 arabidopsis
16	1728	66.6	581	10	Q3YF4 nicotiana t

17	1719	66.3	646	10	Q38870
18	1717.5	66.2	578	10	Q24460
19	1709.5	65.9	573	10	P38388
20	1709	65.9	483	10	Q39014
21	1708	65.9	581	10	Q93YF7
22	1700.5	65.6	484	10	Q9SZM3
23	1672.5	64.5	639	10	Q82107
24	1672.5	64.5	639	10	Q82107
25	1630	63.3	583	10	Q9ZV15
26	1592	61.4	542	10	Q41783
27	1587	61.2	542	10	Q9SNK9
28	1531.5	59.1	548	10	Q9S724
29	1524.5	58.8	548	10	Q9S786
30	1509.5	58.2	528	10	Q8VYE7
31	1506.5	58.1	528	10	Q8VYE7
32	1484.5	57.3	540	10	Q81390
33	1482	57.2	531	10	Q949U0
34	1482	57.2	531	10	Q949U0
35	1480	57.1	518	10	Q9ZSA2
36	1480	57.1	531	10	Q9AXA7
37	1475	56.9	347	10	Q41790
38	1473	56.8	553	10	Q8RW36
39	1471.5	56.7	521	10	Q94KH6
40	1469.5	56.7	542	10	Q9AR92
41	1464.5	56.5	514	10	Q9AR15
42	1463.5	56.4	521	10	Q9C6P3
43	1462	56.4	529	10	Q42479
44	1462	56.4	534	10	Q9FRK2
45	1458.5	56.2	538	10	Q24431

## ALIGNMENTS

RESULT 1

Q39016 PRELIMINARY; PRT; 495 AA.

ID Q39016; AC Q39016; DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Calcium-dependent protein kinase.

OS Arabidopsis thaliana (Mouse-ear cress).

GN Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]\_taxID=3702;

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=94359455; PubMed=8078458;

RA Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,

RA Hayashida N., Shinozaki K.;

RT "Two genes that encode Ca2+-dependent protein kinases are induced by

RT drought and high-salt stresses in Arabidopsis thaliana.";

RL Mol. Gen. Genet. 244:331-340(1994)

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL: D21806; BAAC4830.1; --

DR HSSP; P02593; 1FW4.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR000719; Euk\_pkinase.

DR InterPro; IPR002290; Ser\_thr\_pkinase.

DR Pfam; PF00036; ehand; 4.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk\_pkinase; 1.

DR ProDom; PD000012; EF-hand; 2.

DR SMART; SM00054; EFL; 4.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00108; EF HAND; UNKNOWN 4.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS01008; PROTEIN\_KINASE\_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 495 AA; 55667 MW; 5909A451242C3A6D CRC64;

Query Match 100.0%; Score 2593; DB 10; Length 495;  
Best Local Similarity 100.0%; Pred. No. 9.5e-183;  
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKNPRPNTVLPYOTPLRDHYLLGKKGOGFTTLCSTSTANYACKSIPKR 60  
DB 1 METKNPRPNTVLPYOTPLRDHYLLGKKGOGFTTLCSTSTANYACKSIPKR 60

QY 61 KLVCRDVEDVWREIQMHLSHPNVVRVRIKGTYESVVFVHIVNEVCEGGELFDRIVSKG 120  
DB 61 KLVCRDVEDVWREIQMHLSHPNVVRVRIKGTYESVVFVHIVNEVCEGGELFDRIVSKG 120

QY 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPNFVLDSPKDDAKLKATDFGLSVFYKP 180  
DB 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPNFVLDSPKDDAKLKATDFGLSVFYKP 180

QY 181 GQYLDVVGSPYYVAPEVLKCYGPEIDVMSAGVILVLLSGVPPFWAETESGIFRQILQ 240  
DB 181 GQYLDVVGSPYYVAPEVLKCYGPEIDVMSAGVILVLLSGVPPFWAETESGIFRQILQ 240

QY 241 GKLDKSPDPWPTISAADKLLYKMLSPKRSIAHEALCHPWIVDEQAAPDKPLDPAVL 300  
DB 241 GKLDKSPDPWPTISAADKLLYKMLSPKRSIAHEALCHPWIVDEQAAPDKPLDPAVL 300

QY 301 SRLKQFSQNKIKKQALRVIAERLSEIEIGLKELFKMIDTNSGTTITFEELKAGLKRVG 360  
DB 301 SRLKQFSQNKIKKQALRVIAERLSEIEIGLKELFKMIDTNSGTTITFEELKAGLKRVG 360

QY 361 SELMESEIKSLMDAADIINSCTIDYGFLLAATLHMKNVREELVAFSDFDKGSGYIT 420  
DB 361 SELMESEIKSLMDAADIINSCTIDYGFLLAATLHMKNVREELVAFSDFDKGSGYIT 420

QY 421 IDELOSACTEFGCLCTPLDDMIKIDLDNKGIDFSEFTAMRKGDGVSRTMMKNLNF 480  
DB 421 IDELOSACTEFGCLCTPLDDMIKIDLDNKGIDFSEFTAMRKGDGVSRTMMKNLNF 480

QY 481 NIADAFGVGDEKSD 495  
DB 481 NIADAFGVGDEKSD 495

RESULT 2

Q949P0 PRELIMINARY; PRT; 495 AA.

AC Q949P0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Putative calcium-dependent protein kinase SKS.  
GN F1504.8.

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]\_TaxID=3702;  
RP SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,  
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.B.,  
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Kosuma E., Lam B.,  
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.R.,  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RI Full length cDNA of gene F1504.8 (GI:878378).  
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY050981; AAK93658.1;  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000719; Euk\_pkinase.

DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00036; ehand; 4;  
DR Pfam; PF00069; pkinase; 1;  
DR ProDom; PD000001; Euk\_pkinase; 1;  
DR ProDom; PD000012; EF-hand; 2;  
DR ProSITE; PS00018; EF\_HAND; UNKNOWN 4;  
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1;  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1;  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; UNKNOWN 1;  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 495 AA; 55916 MW; 2DD0ED8C234EF2F7 CRC64;

Query Match 99.4%; Score 2577; DB 10; Length 495;  
Best Local Similarity 99.6%; Pred. No. 1.4e-181;  
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 METKNPRPNTVLPYOTPLRDHYLLGKKGOGFTTLCSTSTANYACKSIPKR 60  
DB 1 METKNPRPNTVLPYOTPLRDHYLLGKKGOGFTTLCSTSTANYACKSIPKR 60

QY 61 KLVCRDVEDVWREIQMHLSHPNVVRVRIKGTYESVVFVHIVNEVCEGGELFDRIVSKG 120  
DB 61 KLVCRDVEDVWREIQMHLSHPNVVRVRIKGTYESVVFVHIVNEVCEGGELFDRIVSKG 120

QY 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPNFVLDSPKDDAKLKATDFGLSVFYKP 180  
DB 121 HFSEREAVKLITLGVVEACHSLGVNHRDLKPNFVLDSPKDDAKLKATDFGLSVFYKP 180

QY 181 GQYLDVVGSPYYVAPEVLKCYGPEIDVMSAGVILVLLSGVPPFWAETESGIFRQILQ 240  
DB 181 GQYLDVVGSPYYVAPEVLKCYGPEIDVMSAGVILVLLSGVPPFWAETESGIFRQILQ 240

QY 241 GKLDKSPDPWPTISAADKLLYKMLSPKRSIAHEALCHPWIVDEQAAPDKPLDPAVL 300  
DB 241 GKLDKSPDPWPTISAADKLLYKMLSPKRSIAHEALCHPWIVDEQAAPDKPLDPAVL 300

QY 301 SRLKQFSQNKIKKQALRVIAERLSEIEIGLKELFKMIDTNSGTTITFEELKAGLKRVG 360  
DB 301 SRLKQFSQNKIKKQALRVIAERLSEIEIGLKELFKMIDTNSGTTITFEELKAGLKRVG 360

QY 361 SELMESEIKSLMDAADIINSCTIDYGFLLAATLHMKNVREELVAFSDFDKGSGYIT 420  
DB 361 SELMESEIKSLMDAADIINSCTIDYGFLLAATLHMKNVREELVAFSDFDKGSGYIT 420

QY 421 IDELOSACTEFGCLCTPLDDMIKIDLDNKGIDFSEFTAMRKGDGVSRTMMKNLNF 480  
DB 421 IDELOSACTEFGCLCTPLDDMIKIDLDNKGIDFSEFTAMRKGDGVSRTMMKNLNF 480

QY 481 NIADAFGVGDEKSD 495  
DB 481 NIADAFGVGDEKSD 495

RESULT 3

Q91QH7 PRELIMINARY; PRT; 557 AA.

AC Q91QH7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE F1504.8.

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]\_TaxID=3702;  
RP SEQUENCE FROM N.A.  
RA Ecker J.R.;  
RI Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY050981; AAK93658.1;  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000719; Euk\_pkinase.

Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

```

[3]
SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C.,
RA Khan S., Kim C., Alafai H., Bai B., Chin C., Chieu J., Choi E., Lam B.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li C., Liu A., Liu J., Liu S., Mukharly N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.,
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC007887; AAF79386.1; -.
DR HSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00017; PROTEIN KINASE ATP; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE-ST; 1.
DR ARP-binding; Serine/threonine-protein kinase; Transferase.
KW
SQ
SEQUENCE 557 AA; 63397 MW; P592BA5A6B3A240B CRC64;

Query Match 97.8%; Score 2536; DB 10; Length 557;
Best Local Similarity 88.5%; Pred. No. 1.8e-178;
Matches 493; Conservative 0; Mismatches 2; Indels 62; Gaps 1;

QY 1 METKPRPSNTLVLYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTANYACKSIPIKR 60
Db 1 METKPRPSNTLVLYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTANYACKSIPIKR 60

QY 61 KLVCREYEDVWEIQTIMHLSHPNVVRIKGTYESVVFHIVMEVCEGGELFDRIVSKG 120
Db 61 KLVCREYEDVWEIQTIMHLSHPNVVRIKGTYESVVFHIVMEVCEGGELFDRIVSKG 120

QY 121 HFSEREAVKLIKTILGVVEACHSLGVHHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKP 180
Db 121 HFSEREAVKLIKTILGVVEACHSLGVHHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKP 180

QY 181 ----- 180
Db 181 GLFLPLWLDLSLILQVFLVFLVPSMNRKLKQSGFLJETGLLCTFIWIANENKVFQMYRFD 240

QY 181 --GOYLYDVVGSPPYVAPELVKCYGPEIDVWAGVILYLLSGVPPFWAETESGIFRQI 238
Db 241 LFGYLYDVVGSPPYVAPELVKCYGPEIDVWAGVILYLLSGVPPFWAETESGIFRQI 300

QY 239 LOGKLDKSPWPPTISAADKLYKMLERSPKKRI SAHREALCHPWVDSQAAAPDKPLDPA 298
Db 301 LOGKLDKSPWPPTISAADKLYKMLERSPKKRI SAHREALCHPWVDSQAAAPDKPLDPA 360

QY 299 VLSRLKQFSQNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKR 358
Db 361 VLSRLKQFSQNKIKKVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKR 420

QY 359 VGSRLMSEIKSLMDAIDNSGTIDYGEFLAATLHNMKEREELIIVAAFSDFDKGSGY 418
Db 421 VGSRLMSEIKSLMDAIDNSGTIDYGEFLAATLHNMKEREELIIVAAFSDFDKGSGY 480

QY 419 ITIDELQSACTEFGICDTPDDMKETDLDNDGKIDFSEPTAMMRKGDGVGRSRTWKNL 478
Db 481 ITIDELQSACTEFGICDTPDDMKETDLDNDGKIDFSEPTAMMRKGDGVGRSRTWKNL 540

QY 479 NFNIADAFGVGDGSKDD 495
Db 541 NFNIADAFGVGDGSKDD 557

```

RESULT 4

```

Q38859
ID Q38869 PRELIMINARY; PRT; 501 AA.
AC Q38869;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calmodulin-domain protein kinase CDPK isoform 4 (Fragment).
GN CPK4 OR T25P22.10 OR AT4G09570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA McCombie W.R.;
RT "Arabidopsis thaliana Genomic Sequence, Chromosome IV.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RP McCombie R.W., Spiegel L.A., Huang E.N., Nascimento L.U.,
RA de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R.,
RA O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H.,
RA Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31752; AAB03243.1; -.
DR EMBL; AL161831; CAB82124.1; -.
DR EMBL; AL161515; CAB78080.1; -.
DR HSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00017; PROTEIN KINASE ATP; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE-ST; 1.
KW Kinase; Serine/threonine-protein kinase.
FT NON_TER 1
SQ
SEQUENCE 501 AA; 56416 MW; C709C17DFAF74B70 CRC64;

Query Match 94.8%; Score 2458; DB 10; Length 501;
Best Local Similarity 94.8%; Pred. No. 8.6e-173;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRPRPSNTLVLYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTANYACKSIPIKR 63
Db 3 KPNRPRPSNTLVLYQTPRLRDHYLLKGLGQGFQGTLYLCTEKSTANYACKSIPIKR 62

QY 64 CREDYEDVWEIQTIMHLSHPNVVRIKGTYESVVFHIVMEVCEGGELFDRIVSKGHS 123
Db 63 CREDYEDVWEIQTIMHLSHPNVVRIKGTYESVVFHIVMEVCEGGELFDRIVSKGHS 122

```

QY 124 EREAVKLIKTILGVVEACHSLGVWHRDLKPNFLDGPDKDAKATDFGLSVFYKPGQY 183  
 DB 123 EREAAKLIKTILGVVEACHSLGVWHRDLKPNFLDGPDKDAKATDFGLSVFYKPGQY 182  
 QY 184 LVDVGSPPYVAPVVKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFQIILQGLK 243  
 DB 183 LVDVGSPPYVAPVVKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFQIILQGLK 242  
 QY 244 DFKSDPWTISBAAXDLIYKMLERSPKKRIISAHEALCHPMIVDEQAAPDKPLDPAVLSRL 303  
 DB 243 DFKSDPWTISBAAXDLIYKMLERSPKKRIISAHEALCHPMIVDEQAAPDKPLDPAVLSRL 302  
 QY 304 KQPSQWKKIYKMLRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFELKAGIKRVGSEL 363  
 DB 303 KQPSQWKKIYKMLRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFELKAGIKRVGSEL 362  
 QY 364 MESEIKSLMDAADIENSNGTIDYGEFLAATLHNKWEREEILVAFSDFDKDGGSYITIDE 423  
 DB 363 MESEIKSLMDAADIENSNGTIDYGEFLAATLHNKWEREEILVAFSDFDKDGGSYITIDE 422  
 QY 424 LOSACTEFLGLDTPDDMIKEIDLNDGKIDFSEFTAMWKGDGVSRTMKNLNFNTA 483  
 DB 423 LOSACTEFLGLDTPDDMIKEIDLNDGKIDFSEFTAMWKGDGVSRTMKNLNFNTA 482  
 QY 484 DAFGVGDG----EKSD 495  
 DB 483 EAFGVEDTSTAKSD 498

## RESULT 5

O24430  
 ID O24430 PRELIMINARY; PRT; 490 AA.  
 AC O24430;  
 DT 01-JAN-1998 (TREMELrel. 05, Created)  
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE Calmodulin-like domain protein kinase isoenzyme beta.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McKendree W.L., Doostdar H., McColm T.G., Mayer R.T.;  
 RT "cDNA cloning and expression of a gene (Accession No. 297064) from  
 citrus paradisi roots similar to bacterial FRN1 and HEA10 proteins  
 and an mRNA from Brassica oleracea that is wound and dark inducible  
 (PGR97-127).";  
 RL Plant Physiol. 115:314-314 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Lee J.-Y., Yoo B.-C., Harmon A.C.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY, BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: U69173; AAB80692.1; -;  
 DR HSP: P02588; IPON.  
 DR InterPro: IPR002048; EF-hand.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00036; ehand; 4;  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000012; EF-hand; 2.  
 DR SMART: SM00054; EHF; 4.  
 DR SMART: SM00220; S\_TK; 1.  
 DR PROSITE: PS00018; EF HAND; UNKNOWN 4.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 490 AA; 55164 MW; 2333C411CAA43E0F CRC64;

Query Match 78.3%; Score 2030; DB 10; Length 490;  
 Best Local Similarity 81.1%; Pred. No. 2 8e-141;  
 Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;  
 QY 14 VLPYQTPRIURDHYLLGKLGQGGQFQTTVLCSTEKSTSNANYACKSIPKPKLVCREDDYDWR 73  
 DB 12 VLPYQTPRIURDHYLLGKLGQGGQFQTTVLCSTEKSTSNANYACKSIPKPKLVCREDDYDWR 71  
 QY 74 EIQIMHHLSEHNVRVRIKGTVEYDSVFVHVMVECGEGELFDRIIVSKGHPSEERAVKLIKT 133  
 DB 72 EIQIMHHLSEHNVRVRIKGTVEYDSVFVHVMVECGEGELFDRIIVSKGHPSEERAVKLIKT 131  
 QY 134 ILGVVEACHSLGVWHRDLKPNFLDGPDKDAKATDFGLSVFYKPGQYILYDVGSPY 193  
 DB 132 ILGVVEACHSLGVWHRDLKPNFLDGPDKDAKATDFGLSVFYKPGQYILYDVGSPY 191  
 QY 194 VAPEVLCKYQGEVDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPMTI 253  
 DB 192 VAPEVLCKYQGEVDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKFSDPMTI 251  
 QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPMIVDEQAAPDKPLDPAVLSRLKQPSQWKKI 313  
 DB 252 SEAAKDLIYKMLERSPKKRIISAHEALCHPMIVDEQAAPDKPLDPAVLSRLKQPSQWKKI 310  
 QY 314 KVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFELKAGIKRVGSELSEIKSLMD 373  
 DB 311 KVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITTFELKAGIKRVGSELSEIKSLMD 370  
 QY 374 AADIDNSGTIDYGEFLAATLHNKWEREEILVAFSDFDKDGGSYITIDELQACTEFL 433  
 DB 371 AADIDNSGTIDYGEFLAATLHNKWEREEILVAFSDFDKDGGSYITIDELQACTEFL 430  
 QY 434 CDTFLDMDIKEIDLNDGKIDFSEFTAMWKGDGVSRTMKNLNFNTA 488  
 DB 431 CDTFLDMDIKEIDLNDGKIDFSEFTAMWKGDGVSRTMKNLNFNTA 486

## RESULT 6

O24319  
 ID O24319 PRELIMINARY; PRT; 496 AA.  
 AC O24319;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE Calcium dependent protein kinase.  
 DE RICDPK2.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-CV, RISHIRI; TISSUE-CELL SUSPENSION;  
 RA Puruchi N., Okita T., Hara N.;  
 RT "Calcium dependent protein kinase genes from resistant and susceptible  
 potato cultivars to Phytophthora infestans.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB051809; BAB63464.1; -;  
 DR InterPro: IPR002048; EF-hand.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00036; ehand; 4;  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000012; EF-hand; 2.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00018; EF HAND; UNKNOWN 4.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.  
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; UNKNOWN 1.  
 KW ATP-binding; Kinase; Transferase.

SQ SEQUENCE 496 AA; 55774 MW; EC41F7AED33B6D5 CRC64;

Query Match 76.0%; Score 1969.5; DB 10; Length 496;  
 Best Local Similarity 76.6%; Pred. No. 8.3e-137;  
 Matches 377; Conservative 55; Mismatches 53; Indels 7; Gaps 4;

QY 1 METKP--NPRRSNTVLPYQTPRLDRHYLLGKLGQGFQTTLYLCTEKSSTANYACKSIP 58  
 DB 1 MEKPKATEPKKSVWLPYKTSQSLQTYTIGKLGQGFQTTLYLCTEKSSTANYACKTIP 60

QY 59 KRLVCREDEYDVRBQIWMHLSHPNVVRIGTYESVFIHMEVCEGGEFDRIVS 118  
 DB 61 KKLI CKEDYEDWKIQLMEHLSHPNVVRIGTYEDYALVHVMELCAGGEFDRIVE 120

QY 119 KHFSREAVKLIKTILGVVEACHSLGVWHRDLKPNFLFDSPKDKAKLKATDGLSVFY 178  
 DB 121 KHYSREAAKLTITVGVVEACHSLGVWHRDLKPNFLFDSDEDAKATDGLSVFY 180

QY 179 KPGQYLDVVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQI 238  
 DB 181 KPGETSDVVGSPYVVAPEVLKCYGHESDVMSAGVILYLLSGVPPFWAETDMGIFRQI 240

QY 239 LQKLPKSPDPWTITSEAAKDLIYKMLSPKRSISAHEALCHPWIVDEQAAPDKPLDPA 298  
 DB 241 LRGLDLSESPWFGISDSAKDLIRKILDRNPKRLTAHEVLCHPWIVDTPVAPDKPLDSA 300

QY 299 VLSRLKQFSQWNIKKWALRVIAERLSEEEIGLKEPKMIDTDSGTTTPEELKAGLKR 358  
 DB 301 VLSRLKQFSANWKLKQWALRVIAERLSEEEIGLKEPKMIDTDSGTTTPEELKEGLRR 360

QY 359 VGSSEMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMKNKEREELVAAFSDFDKGSGY 418  
 DB 361 VGSSEMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMKNKEREELVAAFSDFDKGSGY 420

QY 419 ITDELQSACTEFLCDTPDDMIKEIDLNDGKIDFSEFTAMRKGDG--VGRSRTWVK 476  
 DB 421 ITBELQQAQCKEFLSENLDELKIDQNDGQIDYKFSAMWRKGTGCAVGR-RTNRN 479

QY 477 NLNENIADAFGV 488  
 DB 480 NL--NLGEALGL 489

RESULT 7

Q42396 Q42396 PRELIMINARY; PRT; 490 AA.  
 AC Q42396  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Calcium-dependent protein kinase.  
 GN CDPK9.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Hong Y., Takano M., Liu C.M., Gasch A., Chye M.L., Tan C.T., Koh C.C.,  
 RA Chua N.H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20181125; PubMed=10718197;  
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence  
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC  
 RT clones.";  
 RL DNA Res. 7:31-63(2000).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; U26626; AAA67657.1; -;  
 DR EMBL; U20388; AAA67653.1; -;  
 DR EMBL; AB025633; BAA97242.1; -;  
 DR HSP; P02588; 1PCN.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00036; sfhand; 4;  
 DR Pfam; PF00069; pkinase; 1;  
 DR ProDom; PD000001; Euk\_pkinase; 1;  
 DR ProDom; PD000012; EF-hand; 2;  
 DR SMART; SMO0054; EFh; 4;  
 DR SMART; SMO0220; S\_TKc; 1;  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 4.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 490 AA; 55379 MW; 0315346396585264 CRC64;

Query Match 71.1%; Score 1844.5; DB 10; Length 490;  
 Best Local Similarity 73.1%; Pred. No. 1.3e-127;  
 Matches 353; Conservative 55; Mismatches 68; Indels 7; Gaps 2;

QY 1 METKNPRPSNTVLPYQTPRLDRHYLLGKLGQGFQTTLYLCTEKSSTANYACKSIPKR 60  
 DB 1 MANKPRTR---WLPYKTXNVEDNYFLGVLGQGFQTTFLCTHKTQGLACKSIPKR 56

QY 61 KLVCREDEYDVRBQIWMHLSHPNVVRIGTYESVFIHMEVCEGGEFDRIVSKG 120  
 DB 57 KLVCREDEYDVRBQIWMHLSHPNVVRIGTYESVFIHMEVCEGGEFDRIVKRG 116

QY 121 HFSREAVKLIKTILGVVEACHSLGVWHRDLKPNFLFDSPKDKAKLKATDGLSVFKP 180  
 DB 117 HYSREAAKLIKTIVGVVEACHSLGVWHRDLKPNFLFDSDEDAKSTDFGLSVFQTP 176

QY 181 GOVLYDVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240  
 DB 177 GEAFSELVGSAYVVAPEVLKCYGHESDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 236

QY 241 GKLPKSPDPWTITSEAAKDLIYKMLSPKRSISAHEALCHPWIVDEQAAPDKPLDPAVL 300  
 DB 237 GKLEFEINPWPISSESADLIKKMLSPKRLTAHVLCWPWIVDDKVPDKPLDCAV 296

QY 301 SRLKQFSQWNIKKWALRVIAERLSEEEIGLKEPKMIDTDSGTTTPEELKAGLKEVG 360  
 DB 297 SRLKQFSANWKLKQWALRVIAERLSEEEIGLKEPKMIDTDXSGTTTPEELKDSMRVG 356

QY 361 SELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMKNKEREELVAAFSDFDKGSGYIT 420  
 DB 357 SELMESEIQELLRADVDSEGTIDYGEFLAATLHMKNKEREELVAAFSDFDKGSGYIT 416

QY 421 IDELQSACTEFLCDTPDDMIKEIDLNDGKIDFSEFTAMRKGDGGRS---RTWKN 477  
 DB 417 IEELQQAQCKEFLSENLDELKIDQNDGQIDYGEFVAMWRKGTGGGIGRRTMRS 476

QY 478 LNF 480  
 DB 477 LNF 479

RESULT 8

Q9FXQ3 Q9FXQ3 PRELIMINARY; PRT; 551 AA.  
 AC Q9FXQ3  
 AC Q9FXQ3; 2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE OSCDPK7.  
 GN OSCDPK7.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Eriophytaceae; Oryzae; Oryza.  
 CC NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RX MEDLINE=20387027; PubMed=10929125;  
 RA Saijo Y., Hata S., Koyuka J., Shimamoto K., Izui K.;  
 RT "Over-expression of a single Ca2+-dependent protein kinase confers  
 both cold and salt/drought tolerance on rice plants.";  
 RL Plant J. 23:319-327(2000).  
 DR EMBL; AB042550; BAB16888.1; -.  
 DR HSSP; P02593; 1CTR.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00036; ehand; 4.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR SMART; SM00054; EFh; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 3.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; transferase.  
 SQ SEQUENCE 551 AA; 60966 MW; E479A089EF287A7B CRC64;

Query Match 69.4%; Score 1773; DB 10; Length 551;  
 Best Local Similarity 71.2%; Pred. No. 2.9e-122;  
 Matches 339; Conservative 53; Mismatches 82; Indels 2; Gaps 2;

QY 13 TVLPYOTPLRDLHYLLGKLGQGGFGTTLCTEKSSTANYACKSIKRLKVCREDYEDVW 72  
 DB 75 SVLGHTPTPLRLDYALGRKLGQGGFGTTLCTELSTGVYACKSIKRLKLTIEDVW 134  
 QY 73 REIQIMHLSHNPVVRKIGTYEDSVFVHIVNEVCEGGEFDRIVSKGHFSEAEVKLIK 132  
 DB 135 REIQIMHLSGHKNVVAIKGAYEDQVYVHIVNELCAGGELFDRIIQRGHYSEKAAELTR 194  
 QY 133 TLGVVEACHSLGVHRLKPNELFDSPKDAKLLKATDFGLSVFYKPGGYLDVVGSPY 192  
 DB 195 IIVGVVEACHSLGVHRLKPNELFLANKDDLSLKALDFGLSVFFKPGQTFDVGSPY 254  
 QY 193 YVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLDKFSQDPWPT 252  
 DB 255 YVAPEVLKHYGPEADVWTAGVILYLLSGVPPFWAETQQGIFDAVLKGFIDFSDPWPV 314  
 QY 253 ISBAKDLIVKMLERSPKRIKSAHEALCHPMIVDEQAAPKPLDPAVLRLKQFSQWVKI 312  
 DB 315 ISBAKDLITKMLNPRKRLTAHEVLCHEVLCHEVLCHEVLCHEVLCHEVLCHEVLCHEV 374  
 QY 313 KQALRVIAERLSEBIEIGLKFPMIDTNSGTTTFBELKAGLRKRVGSELMESEIKSLM 372  
 DB 375 KQALRVIAERLSEBIEIGLKFPMIDTNSGTTTFBELKAGLRKRVGSELMESEIKSLM 434  
 QY 373 DAADINSGTIDYGEFLAATLHNMKREELILVAAFSDFDKDGSYITIDELQSACTEFG 432  
 DB 435 DAADINSGTIDYGEFLAATLHNMKREELILVAAFSDFDKDGSYITIDELQSACTEFG 494  
 QY 433 LCOTPLDDMKETDLNDGKIDPSEFTAMRKGD-GVGRSTNMKNLNFNIAAFG 487  
 DB 495 MPDAFLDDVINEADQNDGRIDYGBFVAMTKGNVGVGR-RTMNSLNISNRDAPG 549

RESULT 9  
 O04417 PRELIMINARY; PRT; 492 AA.  
 AC O04417;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)

DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Calcium dependent protein kinase.  
 GN ZMCDPKL  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Zea.  
 ON NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HONEY BANTUM;  
 RA Berberich T., Kusano T.;  
 RT "Cycloheximide induces a subset of low-temperature-inducible genes in  
 maize.";  
 RL Mol. Gen. Genet. 0:0-0(1996).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HONEY BANTUM;  
 RX MEDLINE=97294505; PubMed=9150261;  
 RA Berberich T., Kusano T.;  
 RT "Cycloheximide induces a subset of low temperature-inducible genes in  
 maize.";  
 RL Mol. Gen. Genet. 254:275-283(1997).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; D84408; BAA12338.1; -.  
 DR HSSP; P02593; 1CTR.  
 DR InterPro; IPR002248; EF-hand.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00036; ehand; 4.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR SMART; SM00054; EFh; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN 4.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 492 AA; 54734 MW; 8615C3C360CE949 CRC64;

Query Match 67.6%; Score 1752; DB 10; Length 492;  
 Best Local Similarity 70.6%; Pred. No. 8.7e-121;  
 Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;

QY 13 TVLPYOTPLRDLHYLLGKLGQGGFGTTLCTEKSSTANYACKSIKRLKVCREDYEDVW 72  
 DB 14 SVLGHTPTPLRLDYALGRKLGQGGFGTTLCTELATGIDYACKSIKRLKLTIEDVW 73  
 QY 73 REIQIMHLSHNPVVRKIGTYEDSVFVHIVNEVCEGGEFDRIVSKGHFSEAEVKLIK 132  
 DB 74 REIQIMHLSGHKNVVAIKGAYEDQVYVHIVNELCAGGELFDRIIQRGHYSEKAAELTR 133  
 QY 133 TLGVVEACHSLGVHRLKPNELFDSPKDAKLLKATDFGLSVFYKPGGYLDVVGSPY 192  
 DB 134 IIVGVVEACHSLGVHRLKPNELFLANKDDLSLKALDFGLSVFFKPGQTFDVGSPY 193  
 QY 193 YVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQKLDKFSQDPWPT 252  
 DB 194 YVAPEVLKHYGPEADVWTAGVILYLLSGVPPFWAETQQGIFDAVLKGFIDFSDPWPV 253  
 QY 253 ISBAKDLIVKMLERSPKRIKSAHEALCHPMIVDEQAAPKPLDPAVLRLKQFSQWVKI 312  
 DB 254 ISBAKDLITKMLNPRKRLTAHEVLCHEVLCHEVLCHEVLCHEVLCHEVLCHEVLCHEV 313  
 QY 313 KQALRVIAERLSEBIEIGLKFPMIDTNSGTTTFBELKAGLRKRVGSELMESEIKSLM 372  
 DB 314 KQALRVIAERLSEBIEIGLKFPMIDTNSGTTTFBELKAGLRKRVGSELMESEIKSLM 373  
 QY 373 DAADINSGTIDYGEFLAATLHNMKREELILVAAFSDFDKDGSYITIDELQSACTEFG 432

```

Db 374 DAADINSGTIDYIEFIAATLHLNKLREHILVAAPSYFDKDGSGYITVDLQACKHN 433
QY 433 LCPDPLDDMIKEIDLDNDGKIDFSEPTAMWRKGD-GVGRSRTMMKNLNFNIAD 484
Db 434 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVR-RTMRNSLNSMRD 485

RESULT 10
Q43676 PRELIMINARY; PRT; 487 AA.
AC Q43676;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN CDPK.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=RWILCZ, AND CV. BERKEN; TISSUE=ETIOLATED HYPOCOTYL;
RX MEDLINE=96311003; PubMed=8704124;
RA Botella J.R., Arteca J.M., Somodevilla M., Arteca R.N.;
RT "Calcium-dependent protein kinase gene expression in response to
physical and chemical stimuli in mungbean (Vigna radiata).";
RL Plant Mol. Biol. 30:1129-1137(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U08140; AAC49403.1; -
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00029; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 487 AA; 54700 MW; 54E6FBF5D93AEB2C CRC64;

Query Match 67.5%; Score 1751; DB 10; Length 487;
Best Local Similarity 69.1%; Pred. No. 1e-120;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

QY 14 VLPYQTPRLRDHYLLGKLGQGGQFGTTVLTCTEKSANYACKSIPKRLVCREDYEDVWR 73
Db 12 VLGHKTPNIRDYLTGLRGLGQGGQFGTTVLTCTENSTNEYACKSISKEKLISKEDVEDVR 71

QY 74 EIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGELFDRIIVSKGHFSEREAVKLTK 133
Db 72 EIQIMHLAGHNVIITIKGAYEDQVYHIVMELCGGELFDRIIQRGHYTERKAELTKI 131

QY 134 ILGVVEACHSLGVWHRDLKPNFLFDSFKDPAKLKATDFGLSVFYKPGQVLYDVVGSPYY 193
Db 132 IVGVVEACHSLGVWHRDLKPNFLVNKDDDFSLKATDFGLSVFFKPGQIFTDVVGSPYY 191

QY 194 VAPVLLKCYGPEIDVWSAGVILYLLSGVPFWAETESGIFRQILQGLKDFKSDPWT 253
Db 192 VAPVLLKHYGPEADVWVTAGVILYLLSGVPFWAETQGGIFDAVLKGLDFDSDPWT 251

QY 254 SEAAKOLIVKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNK 313
Db 252 SUSGKDLIKMLCSQPSERLTAHQVLCHPWICENGVAFDRAIDPAVLRLKQFSQMNK 311

QY 314 KVALRVIAERLSEEBEIAGLRMFQAMDTDNGSITFFBELKAGLRVYSGTLKDVIRLME 485

```

```

Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;
QY 6 NPRPSNTVLPYOTPLRDHYLGKLGQGGTGYLTCTEKTSTANYACKSPKRLVCR 65
Db 77 NPDNQAVYLGHTPNIRDIYLSRLKGQGGTGYLTCTEIASGVDYACKSKRKLK 136
QY 66 EDYEDVWREIQIMHHLSEHPNVRIKGTVEDSVFVHVMVECGGELFDRIIVSKGHFSER 125
Db 137 EDVEDVREIQIMHHLAGHSIVTIKGAIEDSLVYHVMELCAGGELFDRIIQRGHYSER 196
QY 126 EAVKLKTIILGVVEACHSLGWMHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQVLY 185
Db 197 KAELTKIIVGVVEACHSLGWMHRDLKPNFLVKNKDDFSKKAIDFGLSVFFKPGQIPT 256
QY 186 DVVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFROILOKLD 245
Db 257 DVVGSPPYVAPEVLKRYGPEADVWTAGVILYLLSGVPPFWAETQGGIFDAVLKGYIDF 316
QY 246 KSDPWPTISEAAKDLIYKMLERSPKXRISEAHEALCHPWIVDSQAAPDKPLDPAVLSRLKQ 305
Db 317 ESDPWPTISDSAKDLIRRLSSKPAERLTAHEVLRHPWICENGVAAPDRALDPAVLSRLKQ 376
QY 306 FSNQNKIKKALRVIAERLSEETGGIKELFKMIDTNSGTITFEELKAGLKRVGSELM 365
Db 377 FSNKMLKQWALKVIAESSEELAGREMFQMDTNSGATTFDELKAGLRKYGSTLKD 436
QY 366 SEIKSLMDAADIDNSGTIDYGEFLAATLHMKNVEREILVAAFSDFDKGSGVITIDELQ 425
Db 437 TEIHDMDAADVDSNGTIDYSEFATLHKLREBEHLVAAFYQDFDKGSGVITIDELQ 496
QY 426 SACTEFLGLCDPTLDDMIKEIDLNDGKIDSEFTAMRKGD-GVGRSRTMMKLNFIAD 484
Db 497 QACVEHGNADYFLEDDIIEVDQNDGKIDYGEFVEMQKGNAGVGR-RTMNSLNISM 555
QY 485 A 485
Db 556 A 556

RESULT 13
Q93XJ0 PRELIMINARY; PRT; 578 AA.
AC Q93XJ0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-WAR-2002 (TRENBLrel. 20, Last annotation update)
DE Calcium dependent protein kinase.
GN RICDPK1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RISHIRI; TISSUE=SUSPENSION CULTURE;
RA Furuichi N., Okuta T., Hara N.;
RT "Calcium dependent protein kinase genes from resistant and susceptible
RT potato cultivars to Phytophthora infestans.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051808; BAB63463.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProSITE; PS00018; EF HAND; UNKNOWN 4.
DR ProSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
DR ProSITE; PS00108; PROTEIN KINASE ST; 1.
DR ProSITE; PS00109; PROTEIN KINASE ST; 1.
DR ProSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 556 AA; 62127 MW; 737FIAD582B45ED CR64;

Query Match 67.2%; Score 1742; DB 10; Length 556;
Best Local Similarity 68.4%; Pred. No. 5.7e-120;

```

SQ SEQUENCE 578 AA; 64779 MW; 1009FF973EB662D2 CRC64;  
Query Match 67.1%; Score 1739.5; DB 10; Length 578;  
Best Local Similarity 67.6%; Pred. No. 9.3e-120;  
Matches 326; Conservative 62; Mismatches 79; Indels 15; Gaps 1;  
QY 2 ETKNPRRP-----SNTVLPYQTPLRDHYLLGKLGQGGFGTTLCTEK 46  
DB 75 EEKEQPKPKPKPAEMKRVSSAGLRTDVLQKTKGNLKEFFSIGKLGQGGFGTTFKCVEX 134  
QY 47 STSANYACKSIPKRLKLVCREDEYDVMREIQIMHHLSEHPNVVRIKGTYESVFIHMEV 106  
DB 135 ATGKEYACKSIAKRLLTDDDDVEDVRREVQIMHHLAGHPHVISIKGAYEDAVAVHVMVEF 194  
QY 107 CEGGELFDRIIVSKGHFSREBAVKLITKILGVVEACHSLGVNHRDLKPNFLFDPKDDAK 166  
DB 195 CAGGELFDRIIQRGHYTERKAAELRTIIVGVVEACHSLGVNHRDLKPNFLFVQKEDSL 254  
QY 167 LKATDFGLSVFVKPGQVLYDVVGSPYVVAPEVLKCKYCPBIDVMSAGVILYLLSGVPPF 226  
DB 255 LKATDFGLSVFVKPGQVLYDVVGSPYVVAPEVLKCKYCPBIDVMSAGVILYLLSGVPPF 314  
QY 227 WAETESGIFRQILOGKLPKSDPWTITSEAAKDIYKMLERSPKKRISAHEALCHPWIVD 286  
DB 315 WAENEOGIEFQVLHGDLDFKSDPWPISSEDAKDLNRRMLVRDPRRLTAHEVLCHPWVQV 374  
QY 287 EQAAPDKPLDPAVLRLKQFSOMNKIKKMLARVIAERLSEEEIGLKEFLPMIDTNSGT 346  
DB 375 DGVAPEKPLDSAVLSRMKQFSAMNKLKMLARVIAESLSEEEIAGLKEMFKMTDNSGQ 434  
QY 347 ITFEELKAGLRVGSLSMESEIKSLMDAADINSQTIIDYGEFLAATLHMNMVEREELVA 406  
DB 435 ITFEELKEGLKRFSGNLKETEYIDLMQAADVNSGTIDYGEFFIAATLHMNKIERQDHLFA 494  
QY 407 AFSDPKDGSVYITIDELQASCTEFLGCDTFLDDMIKETDLDNDGKIDFSEFTAMVRKGD 466  
DB 495 APCYFDKDGSGYITADELQACEEFGIGDVRMEEMIREADQDNDGRIDINEFVAMMQGN 554  
QY 467 GV 468  
DB 555 PV 556

RESULT 14  
Q93YF3 PRELIMINARY; PRT; 578 AA.  
AC Q93YF3  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Calcium-dependent protein kinase 3.  
DE CDPK3.  
GN Nicotiana tabacum (Common tobacco).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21481752; PubMed=11597999;  
RA Roneis T., Ludwig A.A., Martin R., Jones J.D.G.;  
RT "Calcium-dependent protein kinases play an essential role in a plant  
defence response".  
RL ENBO J. 20:5556-5567(2001).  
DR EMBL; AJ344155; CAC82999.1; .  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00036; ehand; 4.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR ProDom; PD000012; EF-hand; 2.  
DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_4.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 578 AA; 64779 MW; 88778B73F85A16B6 CRC64;  
Query Match 66.9%; Score 1733.5; DB 10; Length 578;  
Best Local Similarity 67.4%; Pred. No. 2.6e-119;  
Matches 325; Conservative 62; Mismatches 80; Indels 15; Gaps 1;  
QY 2 ETKNPRRP-----SNTVLPYQTPLRDHYLLGKLGQGGFGTTLCTEK 46  
DB 75 EEKEQPKPKPKPAEMKRVSSAGLRTDVLQKTKGNLKEFFSIGKLGQGGFGTTFKCVEX 134  
QY 47 STSANYACKSIPKRLKLVCREDEYDVMREIQIMHHLSEHPNVVRIKGTYESVFIHMEV 106  
DB 135 ATGKEYACKSIAKRLLTDDDDVEDVRREVQIMHHLAGHPHVISIKGAYEDAVAVHVMVEF 194  
QY 107 CEGGELFDRIIVSKGHFSREBAVKLITKILGVVEACHSLGVNHRDLKPNFLFDPKDDAK 166  
DB 195 CAGGELFDRIIQRGHYTERKAAELRTIIVGVVEACHSLGVNHRDLKPNFLFVQKEDSL 254  
QY 167 LKATDFGLSVFVKPGQVLYDVVGSPYVVAPEVLKCKYCPBIDVMSAGVILYLLSGVPPF 226  
DB 255 LKATDFGLSVFVKPGQVLYDVVGSPYVVAPEVLKCKYCPBIDVMSAGVILYLLSGVPPF 314  
QY 227 WAETESGIFRQILOGKLPKSDPWTITSEAAKDIYKMLERSPKKRISAHEALCHPWIVD 286  
DB 315 WAENEOGIEFQVLHGDLDFKSDPWPISSEDAKDLNRRMLVRDPRRLTAHEVLCHPWVQV 374  
QY 287 EQAAPDKPLDPAVLRLKQFSOMNKIKKMLARVIAERLSEEEIGLKEFLPMIDTNSGT 346  
DB 375 DGVAPEKPLDSAVLSRMKQFSAMNKLKMLARVIAESLSEEEIAGLKEMFKMTDNSGQ 434  
QY 347 ITFEELKAGLRVGSLSMESEIKSLMDAADINSQTIIDYGEFLAATLHMNMVEREELVA 406  
DB 435 ITFEELKAGLRVGSLSMESEIKSLMDAADINSQTIIDYGEFLAATLHMNMVEREELVA 494  
QY 407 AFSDPKDGSVYITIDELQASCTEFLGCDTFLDDMIKETDLDNDGKIDFSEFTAMVRKGD 466  
DB 495 APCYFDKDGSGYITADELQACEEFGIGDVRMEEMIREADQDNDGRIDINEFVAMMQGN 554  
QY 467 GV 468  
DB 555 PV 556

RESULT 15  
Q938872 PRELIMINARY; PRT; 544 AA.  
AC Q938872  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Calmodulin-domain protein kinase CDPK isoform 6.  
GN CPK6 OR F5J6.5.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroids I; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=COLUMBIA;  
RA Krabak E.M., Dickmann L.J., Satterlee J.S., Sussman M.R.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Zhong J.M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE FROM N.A.

```

RC STRAIN=CV. COLUMBIA;
RA Parnell L., McCombie W.R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Zhong J.M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Parnell L.,
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31835; AAB03246.1; -.
DR EMBL; AC02329; AAB86506.1; -.
DR HSSP; P02593; 1CTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002230; Ser_thr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding, Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 544 AA; 61111 MW; EA4F047BEE985E4F CRC64;

Query Match 66.8%; Score 1731; DB 10; Length 544;
Best Local Similarity 68.3%; Pred. No. 3.6e-119;
Matches 328; Conservative 65; Mismatches 85; Indels 2; Gaps 2;

QY 6 NPREFNTVLPYQTFRLRDHYLLGKLGQCGFTTYLCTEKSTSANACKSIPKRLVCR 65
DB 65 NVDNQSVVVLGHKTENIRDLTYLSRKLQCGFTTYLCTDIATGVDYACKSISKRLISK 124

QY 66 EDYEDVREIQIMHLSHNPVRIKGTVEDSVFVHVMVEVCEGGELFDRIYVSKGHFSER 125
DB 125 EDVEDVREIQIMHLSHNPVRIKGTVEDSVFVHVMVEVCEGGELFDRIYVSKGHFSER 184

QY 126 EAVKLITKILGWAEACHSLGWHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLY 185
DB 185 KAELTKIIVGVAEACHSLGWHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLY 244

QY 186 DVGSPYIVAEVLKCKYGPIDVWAGVILYILLSGVPPFWAETSGIFRQLQKLDLF 245
DB 245 DVGSPYIVAEVLKCKYGPIDVWAGVILYILLSGVPPFWAETSGIFRQLQKLDLF 304

QY 246 KSDPWTISEAAKDLIVKMLERSPKKRI SAHEALCHPWIVDEQAAPDKLPDPAVLSRLKQ 305
DB 305 DTDPAFVSDSAKDLIRKMLCSSPSERLTAHEVLRHPWICENGVAEPDRALDPVLSRLKQ 364

QY 306 FSQMKIKKMLRVIAEPLSEEEIGGLKELPKMDTNSGTTIPEELKAGLXVGSLEME 365
DB 365 FSQMKIKKMLRVIAEPLSEEEIGGLKELPKMDTNSGTTIPEELKAGLXVGSLEME 424

QY 366 SEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMEREELVAAPSDFDKGSYVITIDELQ 425
DB 425 TEIRLMEAADVNSGTTIDYGEFLAATLHMNMEREELVAAPSDFDKGSYVITIDELQ 484

QY 426 SACTEFGLCDTFLDPMIKELDNDGKIDFSEFTAMMKGD-GVGRSRTMMKMLNFNIAD 484
DB 485 QSCIEHGMDTFLEDIKEVDQDNDGRIDYEEFVAMVQKGNAGVGR-RTMKNGLNISMMD 543

```

Search completed: February 13, 2003, 21:10:41  
Job time : 77 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 17:41:47 ; Search time 4632 Seconds  
(without alignments)  
10976.382 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

Sequence: 1 gatccgggtacatatcttc.....tataaaagttttgaattcc 1747

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vit.\*
- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1747	100.0	1747	8	ATHCDPKB	D21806 Arabidopsis
2	1711	97.9	1750	8	AY050981	AY050981 Arabidops
3	1515.8	86.8	1519	8	AY113986	AY113986 Arabidops
4	1202.4	68.8	1657	8	ATU31752	U31752 Arabidopsis
5	846.4	47.3	1754	8	GM069173	U69173 Glycine max
6	803.6	46.0	1732	8	AB051809	AB051809 Solanum t
7	756.4	43.3	1768	6	AX077706	AX077706 Sequence
8	756.4	43.3	1768	8	SOYCADPK	M64987 Glycine max
9	744.2	42.6	1693	8	ATACDPK9	U20388 Arabidopsis
10	712.6	40.8	2036	8	ATU31835	U31835 Arabidopsis
11	706.2	40.4	1858	8	ATHATCDPK	D28582 Arabidopsis
12	698.4	40.0	2393	8	AB051808	AB051808 Solanum t
13	696.8	39.9	2437	8	NTA344155	AJ344155 Nicotiana
14	688.4	39.4	1967	8	ATU31834	U31834 Arabidopsis
15	666.2	38.1	158096	8	AC007887	AC007887 Genomic s
16	666	38.1	2019	8	NTA344154	AJ344154 Nicotiana
17	657.6	37.6	2270	8	AY072801	AY072801 Cucurbita
18	652.6	37.4	2550	6	AX077715	AX077715 Sequence
19	652.6	37.4	2550	8	CPU90262	U90262 Cucurbita p
20	652.2	37.3	1746	8	NBE344156	AJ344156 Nicotiana
21	649.4	37.2	2126	8	AB042550	AB042550 Oryza sat
22	649	37.1	2214	8	AY072802	AY072802 Cucurbita
23	645	36.9	2214	8	ATHCALIIPR	L14771 Arabidopsis
24	643.4	36.8	1857	8	D84408	D84408 Maize mRNA
25	641.8	36.7	2142	8	ATU31833	U31833 Arabidopsis
26	629.8	36.1	2022	6	AX077717	AX077717 Sequence
27	629.8	36.1	2022	8	VRU08140	U08140 Vigna radia
28	625	35.8	2248	8	D87042	D87042 Zea mays mr
29	619.4	35.5	2243	8	TRU82087	U82087 Tortula rur
30	596.2	34.1	1041	8	AY030280	AY030280 Psophocar
31	571.4	32.7	2334	6	AX077709	AX077709 Sequence
32	571.4	32.7	2334	8	OSCDPKENA	X81393 O. sativa mr
33	568.2	32.5	2552	8	AF048691	AF048691 Oryza sat
34	558.8	32.0	1997	8	AY050891	AY050891 Arabidops
35	555.4	31.8	1696	8	AY063004	AY063004 Arabidops
36	555.4	31.8	1975	8	AY034995	AY034995 Arabidops
37	552.4	31.6	1862	8	MSCDPK	X96723 M. sativa mr
38	551	31.5	1998	8	ATU31751	U31751 Arabidopsis
39	551	31.5	2093	8	AY120727	AY120727 Arabidops
40	551	31.5	2566	8	ZMA7366	AJ007366 Zea mays
41	543.6	31.1	1353	8	MZECDPK	L15390 Zea mays ca
42	537.2	30.7	1910	6	AX077707	AX077707 Sequence
43	537.2	30.7	1910	8	D87707	D87707 Sweet potat
44	531.8	30.4	2230	6	AX280992	AX280992 Sequence
45	527.6	30.2	1915	8	AY027885	AY027885 Cucumis s

ALIGNMENTS

RESULT 1  
ATHCDPKB  
LOCUS Arabidopsis thaliana mRNA for calcium-dependent protein kinase  
DEFINITION (CDPK), complete cds.  
1747 bp mRNA linear PLN 05-FEB-1999

ACCESSION D21806  
VERSION D21806.1  
KEYWORDS calcium-dependent protein kinase; ATCDPK2.  
SOURCE Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 1747)  
AUTHORS Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K.,

Db	361	TTTGTTTCATATTGTTATGAGAGTTTGGAAGGGTGGAGCTTTTGTATCGAATGTCTT	420
Qy	421	AAAGTCATTTTAGTGAAGCGTGAAGCTGCTAAGCTTATTAAGACGATCTCTGGTGTGTT	480
Db	421	AAAGTCATTTTAGTGAAGCGTGAAGCTGCTAAGCTTATTAAGACGATCTCTGGTGTGTT	480
Qy	481	GAGGCTTGTCATCTCTCTGGTGTATGTCATAGAGATCTAAACCTGAGAAATTTCTTGTTT	540
Db	481	GAGGCTTGTCATCTCTCTGGTGTATGTCATAGAGATCTAAACCTGAGAAATTTCTTGTTT	540
Qy	541	GATAGTCCTAAAGATGATGCTTAAGCTTAAGGCTACCGAATTTTGGTTTGTCTGCTCTAT	600
Db	541	GATAGTCCTAAAGATGATGCTTAAGCTTAAGGCTACCGAATTTTGGTTTGTCTGCTCTAT	600

Qy	601	AAGCCAGGACAAATATTATATGACGTAGTTGGAAAGTCGCTACTATGTTGCACACAGAGTG	650
Db	601	AAGCCAGGACAAATATTATATGACGTAGTTGGAAAGTCGCTACTATGTTGCACACAGAGTG	650
Qy	661	CTAAGAAATGTTATGGACCTGGAATAGATGTTGGAGTGCTGGTGTTATCCCTCTACATT	720
Db	661	CTAAGAAATGTTATGGACCTGGAATAGATGTTGGAGTGCTGGTGTTATCCCTCTACATT	720
Qy	721	TTACTCAGCGGTGTTCTCCCTCTCTGGCAGAGACTCAGTCTGGAATCTTTAGACAGATA	780
Db	721	TTACTCAGCGGTGTTCTCCCTCTCTGGCAGAGACTCAGTCTGGAATCTTTAGACAGATA	780
Qy	781	TTGCAAGGAACTTAGATTTCAATCTGCACCGTGGCCTACTATCTCAGAGAGCTGCTAAA	840
Db	781	TTGCAAGGAACTTAGATTTCAATCTGCACCGTGGCCTACTATCTCAGAGAGCTGCTAAA	840
Qy	841	GATTTTGATCTATAAAATGCTCGAAGGAGGCCCAAGAAACGCATTTCTGCTCATGAAGCC	900
Db	841	GATTTTGATCTATAAAATGCTCGAAGGAGGCCCAAGAAACGCATTTCTGCTCATGAAGCC	900
Qy	901	TTGTGTCACCCATGATTTGATGAACAAGCAGCACACAGACCTCTTTGATCCAGCA	960
Db	901	TTGTGTCACCCATGATTTGATGAACAAGCAGCACACAGACCTCTTTGATCCAGCA	960
Qy	961	GTCCTATCTCGTCTAAAGCAGTTTTCTCAATAGATTAAGATTAAAGAAAATGGCATTTACGG	1020
Db	961	GTCCTATCTCGTCTAAAGCAGTTTTCTCAATAGATTAAGATTAAAGAAAATGGCATTTACGG	1020

QY	1021	GTAAATGCTTGAGAGACATTCAGAGAGAGAAATGGAGGCTGGAAGGAATTTGTTCAAGATG	1081
Db	1021	GTAAATGCTTGAGAGACTTTCAGAGGAGAAATTCAGAGTCTGAAGGAAATTTGTTCAAGATG	1080
QY	1081	ATAGACACAGACCAACAGCGGAAACGATTACTTTTCAAGAGCTCAAAGCGGGTTTTGAAGAGA	1140
Db	1081	ATAGACACAGACCAACAGCGGAAACGATTACTTTTGAAGAGCTCAAAGCGGGTTTTGAAGAGA	1140
QY	1141	GTCCGATCTGAATCGATGGAAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAC	1200
Db	1141	GTCCGATCTGAATCGATGGAAATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAC	1200
QY	1201	AACAGTGGTACAAATAGACTACGGAGAAATTCCTAGCAGCAACCTTTACACATGAACAAGATG	1260
Db	1201	AACAGTGGTACAAATAGACTACGGAGAAATTCCTATCAGCAACCTTTACACATGAACAAGATG	1260
QY	1261	GAGAGAGGAGATTTCTGGTGGCTGCATTTTCGGACTTTGACAAAGACGGAACGGTTAT	1320
Db	1261	GAGAGAGGAGATTTCTGGTGGCTGCATTTTCGGACTTTGACAAAGACGGAACGGTTAT	1320
QY	1321	ATCACCATCGATGAGCTTCAGTCAGCTTGCAACAGAGTTGGTCTATGTGATACACCTCTG	1380
Db	1321	ATCACCATCGATGAGCTTCAGTCAGCTTGCAACAGAGTTGGTCTATGTGATACACCTCTG	1380
QY	1381	GACGACATGATCAAGAGATTTGATCTTTGACAAATGACGGGAAGATCGATTTCTCGGAGTTT	1440
Db	1381	GACGACATGATCAAGAGATTTGATCTTTGACAAATGACGGGAAGATTCGATTTCTCGGAGTTT	1440
QY	1441	ACAGCAATGATCAGGAAAGGAGATGGAGTTGGGAGAAAGCAACCATGATGAAGAACTTG	1500
Db	1441	ACAGCAATGATCAGGAAAGGAGATGGAGTTTGGGAGAAAGCAGACCAATGATGAAGAACTTG	1500

QY 1501 AACTCAACATCTGATGCTTTGGAGTTGATGCTGAATAATCTGATGACTGACTCATC 1560  
 Db 1501 AACTCAACATCTGATGCTTTGGAGTTGATGCTGAATAATCTGATGACTGACTCATC 1560  
 QY 1561 ATTCCTCCCAATTTCTGTTTTTCTCTTTAAATTCGTTTATATTTGAATTTCTAATT 1620  
 Db 1561 ATTCCTCCCAATTTCTGTTTTTCTCTTTAAATTCGTTTATATTTGAATTTCTAATT 1620  
 QY 1621 TCTAAGGATACAAAATATATCTGCTGTTTTTTGCTTTTCTCTTTTATATTTTGTATCAT 1680  
 Db 1621 TCTAAGGATACAAAATATATCTGCTGTTTTTTGCTTTTCTCTTTTATATTTTGTATCAT 1680  
 QY 1681 GAGCAACTTCTAAATTTTATCTCATATGATGATAATTTTGTCTTCATATAAAAGTTTTT 1740  
 Db 1681 GAGCAACTTCTAAATTTTATCTCATATGATGATAATTTTGTCTTCATATAAAAGTTTTT 1740  
 QY 1741 GAATTC 1747  
 Db 1741 GAATTC 1747

RESULT 2  
 AY050981  
 LOCUS Arabidopsis thaliana putative calcium-dependent protein kinase  
 DEFINITION (Atlg35670) mRNA, complete cds.  
 ACCESSION AY050981  
 VERSION AY050981.1 GI:15293094  
 KEYWORDS FLI CDNA.  
 SOURCE Arabidopsis thaliana.  
 ORGANISM Arabidopsis thaliana.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 1750)  
 Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,  
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,  
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,  
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,  
 Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,  
 Davis,J.R. and Theologis,A.  
 Arabidopsis Full Length cDNA Clones  
 Unpublished  
 2 (bases 1 to 1750)  
 Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M.,  
 Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L.,  
 Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,  
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C.,  
 Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M.,  
 Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,  
 Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and  
 Theologis,A.  
 Direct Submission  
 Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan  
 Street, Albany, CA 94710, USA  
 TITLE Arabidopsis Full-length cDNA : 'RIKEN  
 JOURNAL RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RFLP cDNAs (RFLP cDNA : 'RIKEN  
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PCEC (SSP) Consortium members carried out the  
 sequencing and annotation of the RFLP cDNAs: Yamada,K., Liu,S.X.,  
 Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D.,  
 Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,  
 Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H.,  
 Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B.,  
 Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,  
 Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PCEC) and Seki,M. (RIKEN GSC) contributed equally to  
 this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PCEC)  
 contributed equally to this work as PIs.

FEATURES  
 Location/Qualifiers  
 1..1750  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
 /chromosome="1"  
 /clone="RAPL07-07-K16 (R10736)"  
 /note="This clone is in a modified pBluescript vector  
 (FLC-1) as a BamHI/XhoI insert."  
 ecotype: Columbia  
 1..1750  
 /gene="Atlg35670"  
 1..75  
 /gene="Atlg35670"  
 76..1563  
 /gene="Atlg35670"  
 /note="contains a protein kinase PF00069 domain and  
 contains 4 EF hand PF00036 domains"  
 /codon\_start=1  
 /evidence=experimental  
 /product="putative calcium-dependent protein kinase"  
 /protein\_id="AAK93568.1"  
 /db\_xref="GI:15293095"  
 /translation="METKPNRPSPNTVLPTQLRDHVLGKLGOGFGTTLCT  
 EKSTANACKSIPRKLVCREDEYEDVREIQIMHLSHPNVVRKGYEDSVFVH  
 VMEYEGGELFDRIVSKVGHSEAEVKILIGVVEACHSLGVMRDLPKFLPDS  
 PKDAKLTADFGLSVFYKQYLDVQSPYVPAPELVKCKYCPEDVWSAGVLIYI  
 LLSGVPPFWABTESGI FQIQLQKLPDFKSDPWTI SEAAKDLIYKRLSPKRIISAH  
 BALCPWIVDEOAAAPDPLPAVLRKQFQSNMKIKMALARVIAERLSEETGGKLE  
 LFKMIDTNSGTTIFELKAGLRVSGELMESIKSLMDAADIDNSGTTDYGFLAAT  
 LHYNMREENLVAAFSYFPKDSGYITIDELQSACTEGLCDTPDDMIKEIDLND  
 GKIDFSFTNMRKGGVGRSRKTNKLNFIADAFGVGGEKSDD"  
 1564..1750  
 /gene="Atlg35670"  
 misc\_difference 1734  
 /gene="Atlg35670"  
 /note="not present in genomic sequence"  
 BASE COUNT 533 a 314 c 388 g 515 t  
 ORIGIN  
 Query Match 97.9%; Score 1711; DB 8; Length 1750;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1717; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 8 GTACATATCTTCTTCTTCTTCAATTCGAGATCGAGAACCAACCAACCAACCAACCA 67  
 Db 17 GTTATCATCTTCTTCTTCTTCTTCAATTCGAGATCGAGAACCAACCAACCAACCA 76  
 QY 68 TGGAGACGAGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 127  
 Db 77 TGGAGACGAGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 136  
 QY 128 GATTAGAGATCATTTACCTTCTGGGAAAAAAGCTAGGCAAGGCCAATTTGGAAACCACT 187  
 Db 137 GATTAGAGATCATTTACCTTCTGGGAAAAAAGCTAGGCAAGGCCAATTTGGAAACCACT 196  
 QY 188 ATCTCTGCACAGAGAAATCAACCTCGCTTAATTAGCTGCAAAATCGATCCCGAAGCGAA 247  
 Db 197 ATCTCTGCACAGAGAAATCAACCTCGCTTAATTAGCTGCAAAATCGATCCCGAAGCGAA 256  
 QY 248 AGCTCGTGTGCGGAGGATTACGAAGATGATGCGGTGAGATTCAGATTCATGATCATC 307  
 Db 257 AGCTCGTGTGCGGAGGATTACGAAGATGATGCGGTGAGATTCAGATTCATGATCATC 316  
 QY 308 TCTCTGAGCATCAATGTTGTTAGGATCAAGGACCTTATGAGATTCGGTGTGTTGTC 367  
 Db 317 TCTCTGAGCATCAATGTTGTTAGGATCAAGGACCTTATGAGATTCGGTGTGTTGTC 376  
 QY 368 ATATTTGTTATGGAGGTTTCTGAAGTGGTGAGCTTTTTTGATCGGATTTCTTAAAGTC 427  
 Db 377 ATATTTGTTATGGAGGTTTCTGAAGTGGTGAGCTTTTTTGATCGGATTTCTTAAAGTC 436

QY 428 ATTTTGTAGTGGCTGAGCTGCTCAAGCTTATTAAGACGATTCCTGGTCTTGTGAGGCTT 487  
Db 437 ATTTTGTAGTGGCTGAGCTGCTCAAGCTTATTAAGACGATTCCTGGTCTTGTGAGGCTT 496  
QY 488 GTCAATTCCTCTGTTGTTATGTCATAGAGATCTCAAAACCTCGAGAATTCCTGTTGATAGTC 547  
Db 497 GTCAATTCCTCTGTTGTTATGTCATAGAGATCTCAAAACCTCGAGAATTCCTGTTGATAGTC 556  
QY 548 CTAAGAATGATGCTAAGCTTAAGCTTACGATTTGGTTGTCCTGCTCTCTATTAAGCCAG 607  
Db 557 CTAAGAATGATGCTAAGCTTAAGCTTACGATTTGGTTGTCCTCTCTATTAAGCCAG 616  
QY 608 GACAATATTTATATGACGTAGTTGGAAGTCCGCTACTATGTCACACGAGGCTCAAGA 667  
Db 617 GACAATATTTATGACGTAGTTGGAAGTCCGCTACTATGTCACACGAGGCTCAAGA 676  
QY 668 AATGTTATGACCTGAATAGATGTTGGAGTCTGGTGTATCTCTTACATTTACTCA 727  
Db 677 AATGTTATGACCTGAATAGATGTTGGAGTCTGGTGTATCTCTTACATTTACTCA 736  
QY 728 GCGGTGTTCTCCCTCTCGGACGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAG 787  
Db 737 GCGGTGTTCTCCCTCTCGGACGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAG 796  
QY 788 GGAAGTTAGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTGA 847  
Db 797 GGAAGTTAGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTGA 856  
QY 848 TCTATAAATGCTCGAAGAGAGCCCAAGAAACGCAATCTGCTCATGAAGCTTGTGTC 907  
Db 857 TCTATAAATGCTCGAAGAGAGCCCAAGAAACGCAATCTGCTCATGAAGCTTGTGTC 916  
QY 908 ACCATGATTTGTCATGAACAGACGACAGCAAGGCTTGTATCAGCAGCTTTAT 967  
Db 917 ACCATGATTTGTCATGAACAGACGACAGCAAGGCTTGTATCAGCAGCTTTAT 976  
QY 968 CTCGCTTAAGCAGTTTCTCAATGATTAAGATTAAGAAATGGCATTCAGGGTAATTG 1027  
Db 977 CTCGCTTAAGCAGTTTCTCAATGATTAAGATTAAGAAATGGCATTCAGGGTAATTG 1036  
QY 1028 CTGAGAGACTTTAGAGAGAAATTTGAGTCTGAAGGAATTTGTTCAAGATGATAGACA 1087  
Db 1037 CTGAGAGACTTTAGAGAGAAATTTGAGTCTGAAGGAATTTGTTCAAGATGATAGACA 1096  
QY 1088 CAGACACAGCGGACGATTTCTGAGAGCTCAAGCGGTTTCAAGAGAGTGGAT 1147  
Db 1097 CAGACACAGCGGACGATTTCTGAGAGCTCAAGCGGTTTCAAGAGAGTGGAT 1156  
QY 1148 CTGAATGATGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAAACAGTG 1207  
Db 1157 CTGAATGATGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAAACAGTG 1216  
QY 1208 GTACAATGACTACGAGAAATTCCTAGCAGCAACCTTACATGACAAAGATGGAGAG 1267  
Db 1217 GTACAATGACTACGAGAAATTCCTAGCAGCAACCTTACATGACAAAGATGGAGAG 1276  
QY 1268 AGGAGATTTCTGGTGGCTGATTTTCGGACTTTGCAAAAGACGGAAGCGGTTATATCACCA 1327  
Db 1277 AGGAGATTTCTGGTGGCTGATTTTCGGACTTTGCAAAAGACGGAAGCGGTTATATCACCA 1336  
QY 1328 TCATGAGCTTCAAGTCAAGTTCGACAGAGTTGGTCTATGATACACCTCTCGACAGACA 1387  
Db 1337 TCATGAGCTTCAAGTCAAGTTCGACAGAGTTGGTCTATGATACACCTCTCGACAGACA 1396  
QY 1388 TGATCAGGAGATTGATCTTGAATATGCGGAAGATCGATTCTCGGAGTTTACAGCAA 1447  
Db 1397 TGATCAGGAGATTGATCTTGAATATGCGGAAGATCGATTCTCGGAGTTTACAGCAA 1456  
QY 1448 TGATCAGGAAAGGAGATGGAGTTGGAGAGCAGAAACCATGATGAAGAACTTGAACITCA 1507  
Db 1457 TGATCAGGAAAGGAGATGGAGTTGGAGAGCAGAAACCATGATGAAGAACTTGAACITCA 1516

QY 1508 ACATTCGTGATGCTTTTGGAGTTGATGTTGAAATACTGATGACTGACTCATCTTCTC 1567  
Db 1517 ACATTCGTGATGCTTTTGGAGTTGATGTTGAAATACTGATGACTGACTCATCTTCTC 1576  
QY 1568 CACAAATTTCTGTTTTTTTCTCTTAATTTGCTTTATATTTTGAATTTCTAATTTCTAAGG 1627  
Db 1577 CACAAATTTCTGTTTTTTTCTCTTAATTTGCTTTATATTTTGAATTTCTAATTTCTAAGG 1636  
QY 1628 ATACAAAATATATCTCGCTGCTGTTTTTGGCTTTCTCTTTTATTTTGTACATGAGCAAC 1687  
Db 1637 ATACAAAATATATCTCGCTGCTGTTTTTGGCTTTCTCTTTTATTTTGTACATGAGCAAC 1696  
QY 1688 TTCTTAATTTTATCTCTCATATGATTAATTTTGGCTTCATATAAAA 1734  
Db 1697 TTCTTAATTTTATCTCTCATATGATTAATTTTGGCTTCATATAAAA 1743

RESULT 3  
AY113986 1519 bp mRNA linear PLN 31-MAY-2002  
LOCUS Arabidopsis thaliana putative calcium-dependent protein kinase  
DEFINITION (Atg935670) mRNA, complete cds.  
ACCESSION AY113986  
VERSION AY113986.1 GI:21281140  
KEYWORDS FLI CDNA.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.s.  
REFERENCE 1 (bases 1 to 1519)  
AUTHORS Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,  
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,  
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,  
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,  
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,  
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,  
Davis,R.W., Ecker,J.R. and Theologis,A.  
TITLE Arabidopsis Open Reading Frame (ORF) Clones  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1519)  
AUTHORS Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,  
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,  
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,  
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,  
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,  
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,  
Davis,R.W., Ecker,J.R. and Theologis,A.  
TITLE Direct Submission  
JOURNAL Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
COMMENT The RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA : RIKEN  
Arabidopsis Full-length cDNA): Seki,M., Narusaka,M., Ishida,J.,  
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,  
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and  
sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,  
Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,  
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,  
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,  
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,  
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Shinn,P.,  
Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally  
to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP  
/PGEC) contributed equally to this work as PIs.

FEATURES  
Location/Qualifiers  
1..1519  
source

```

/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
/clone="U10736"
/note="This clone is in pUNI 51.
ecotype: Columbia"

```

```

gene
1. .1519
/gene="At1g35670"
CDS
1. .1488
/
```

```

/genes="At1g35670"
/note="contains a protein kinase PF00069 domain and
contains 4 EF hand PF00036 domains"
/codon start=1

```

```
/evidence=experimental
```

product: putative calcium-dependent protein kinase  
protein\_id: "AAW45034.1"  
/db\_xref="GI:21281141"  
/translation: "METKNRPPSNVLPYQTPRLRDHYLGKLGQQGQFQ  
EKSTNSYACKGIPKGLVCRVDYEDVKEI QIMHLSHPNVRV KGYTVR  
NEVCYBEGSGLFTR ISKSGHVSREAVKL KTIIGVHSCVGLVWRHDKLP  
PDOKAKLDFGLSVFYPKGVLYDVQSPYPAPELVKCYGEEIDVMS  
LISGPPVFAEVBEGSIFVQI LQKLDGFGPMPTISEAKDILYKMLERSPI  
EALCPWIVDEQAPGAPLPAVLRSGLKQVSGMKNIKKALYVARISEEREE  
LFHWIDTNSGTPITREELKAGLRVCSLEWESIEIKSLMAADI DNGSTIDY  
LHMVKEERENLVAAFSYPSKDSQGYITDELQSCATFGLCDTPLDDMKI  
KIKESSEETAMPKPGVCGSPSPMMKNVNIENLDAEGVGGKSD"

3' UTR  
1489. 1519

BASE COUNT	448 a	279 c	366 g	426 t
/gene="ATG35670"				

```

Query Match          86.8%; Score 1515.8; DB 8; Length 1519;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY	67	ATGGAGCGAAGCCAAACCCCTAGAGCTCTTCAAACACAGTTCTACCATATCAACACCA	126
DB	1	ATGGAGACGAGCGCAAACCTTAGAGCTCTTCAAACACAGTTCTACCATATCAACACCA	50
QY	127	CGATTAAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGCCAAGCCAAATTTGGAACAACC	186
DB	61	CGATTAAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGCCAAGCCAAATTTGGAACAACC	120
QY	187	TATCTCTGCACAGAGAATCAACCTCCGCTAAATTCAGCCTGCAAATCGATCCCGAAGCGA	246
DB	121	TATCTCTGCACAGAGAATCAACCTCCGCTAAATTCAGCCTGCAAATCGATCCCGAAGCGA	180
QY	247	AAGCTCGTGTGCGGAGGATTCGAAGATCATATGGCGTGAGATTCAGATCATCATCAT	306
DB	181	AAGCTCGTGTGCGGAGGATTCGAAGATCATATGGCGTGAGATTCAGATCATCATCAT	240
QY	307	CTCTCTGAGCATCCAAATCTTGTTAGGATCAAGGGACTTATGAAGATTCGGTGTTGTT	366
DB	241	CTCTCTGAGCATCCAAATCTTGTTAGGATCAAGGGACTTATGAAGATTCGGTGTTGTT	300
QY	367	CATATTGTTATGGAGGTTTGTGAAGGTGGTGAGCTTTTGTATCGAATTGTTCTAAAGGT	426
DB	301	CATATTGTTATGGAGGTTTGTGAAGGTGGTGAGCTTTTGTATCGAATTGTTCTAAAGGT	360
QY	427	CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAAGCGATTTCTTGCTGTTGTAGGCT	486
DB	361	CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAAGCGATTTCTTGCTGTTGTAGGCT	420
QY	487	TGTCATTCTCTTGCTGTATTGCATAGATCTCAAACCTGAGAATTTCTTGTGTGATAGT	546
DB	421	TGTCATTCTCTTGCTGTATTGCATAGATCTCAAACCTGAGAATTTCTTGTGTGATAGT	480
QY	547	CCTAAGATGATGCTTAAGCTTAAGCTACCGATTTTGCTTGTCTGCTCTCTATAGCCA	606
DB	481	CCTAAGATGATGCTTAAGCTTAAGCTACCGATTTTGCTTGTCTCTCTATAGCCA	540
QY	607	GGACAAATATTATATGACCTAGTTGGAAGTCGCTACTATGTTGCACACAGAGGTGCTAAAG	666

541	DB	GGACAATATTATATGACGTAGTTGGAAAGTCGGTACTACTGTTGCCACGAGGTGCTAAAG	600
667	QY	AAATGTTATGGACCTGAAATAGATGTTGTGAGTGTGGTGGTGTATCTCTCAAGATTTTACTC	726
601	DB	AAATGTTATGGACCTGAAATAGATGTTGTGAGTGTGGTGGTGTATCTCTCAAGATTTTACTC	660
727	QY	ACGGTGTTCCTCCCTCTCGGACGAGACTGAGTCTGGAACTCTTTAGACAGATATTGCAA	786
661	DB	ACGGTGTTCCTCCCTCTCGGACGAGACTGAGTCTGGAACTCTTTAGACAGATATTGCAA	720
787	QY	GGAAAGTTAGATTTCAAATCTGACCCGTGGCCTACTATCTCAGAAGCTGCTAAGATTTG	846
721	DB	GGAAAGTTAGATTTCAAATCTGACCCGTGGCCTACTATCTCAGAAGCTGCTAAGATTTG	780
847	QY	ATCTATAAAATGCTCGAAAGGAGGCCCAAGAAACGCAATTCCTGCTCATGAAGCCTTGCT	906
781	DB	ATCTATAAAATGCTCGAAAGGAGGCCCAAGAAACGCAATTCCTGCTCATGAAGCCTTGCT	840
907	QY	CACCATGGATGTGATGAAGAACAGACAGACACAGAGCTCTTGATCCAGAGTCTTTA	966
841	DB	CACCATGGATGTGATGAAGAACAGACAGACACAGAGCTCTTGATCCAGAGTCTTTA	900
967	QY	TCTCGTCTAAAGCAGTTTCTCAAATGAATAGAAATTAAGAAAAATGCAATACGGGTAAAT	1026
901	DB	TCTCGTCTAAAGCAGTTTCTCAAATGAATAGAAATTAAGAAAAATGCAATACGGGTAAAT	960
1027	QY	GCTGAGAGACTTTGAGAGAAAGAAATTTGGAGGTCTGAGGAATTTGTTCAAGATGATAGAC	1086
961	DB	GCTGAGAGACTTTGAGAGAAAGAAATTTGGAGGTCTGAGGAATTTGTTCAAGATGATAGAC	1020
1087	QY	ACAGACACAGCGGAACGATTTACTTTTGAAGAGCTCAAAGCGGTTTGAAGAGAGTCGGA	1146
1021	DB	ACAGACACAGCGGAACGATTTACTTTTGAAGAGCTCAAAGCGGTTTGAAGAGAGTCGGA	1080
1147	QY	TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACAACAGT	1206
1081	DB	TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGACAACAGT	1140
1207	QY	GGTACAAATAGACTACGGAGAAATTCCTAGCAGACACTTTACACATGAACAAAGATGGAGAGA	1266
1141	DB	GGTACAAATAGACTACGGAGAAATTCCTAGCAGACACTTTACACATGAACAAAGATGGAGAGA	1200
1267	QY	GAGGAGATTCCTGGTGGCTGCATTTTCGGAATTTGCACAAAGACGGAAGCGTTATATCACC	1326
1201	DB	GAGGAGATTCCTGGTGGCTGCATTTTCGGAATTTGCACAAAGACGGAAGCGTTATATCACC	1260
1327	QY	ATCGATGACCTTCAGTCAGCTTCACAGAGTTTGGTCTATGTGATACACCTCTGGACGAC	1386
1261	DB	ATCGATGACCTTCAGTCAGCTTCGACAGAGTTTGGTCTATGTGATACACCTCTGGACGAC	1320
1387	QY	ATCATCAAGAGATTTGATCTTGACAAATGACGGGAAGATTCGATTTTCTCGGAGTTTACAGCA	1446
1321	DB	ATCATCAAGAGATTTGATCTTGACAAATGACGGGAAGATTCGATTTTCTCGGAGTTTACAGCA	1380
1447	QY	ATGATGAGAAAGGAGATGGAGTTGGGAGAGACGAAACCATGATGAAGAACTTGAACCTC	1506
1381	DB	ATGATGAGAAAGGAGATGGAGTTGGGAGAGACGAAACCATGATGAAGAACTTGAACCTC	1440
1507	QY	AACATTCGTGATGCTTTTCGGAGTTGATCGGTGAAAAAATCTGATGACTGACATCATCTTT	1566
1441	DB	AACATTCGTGATGCTTTTCGGAGTTGATCGGTGAAAAAATCTGATGACTGACATCATCTTT	1500
1567	QY	CCACAATTTCTGTTTTTTTTT	1585
1501	DB	CCACAATTTCTGTTTTTTTTT	1519

RESULT 4	
ATU31752	
LOCUS	1657 bp mRNA linear PLN 23-AUG-2001
DEFINITION	Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 4 (CPK4) mRNA, partial cds.
ACCESSION	U31752



QY	162	AGGCCAAGGCCAAATTGGACAACTATCTCTGCACAGAGAAATCAACCTCCGCTAAATTA	221
Db	146	GGGGCAAGGGCAATTTCGGACGAGGTACTGTGCACCAAGGTGACGGGAAGCTCTA	205
QY	222	CGCCTGCAAAATCGATCCCGAAGCAAAAGCTCGTGTGCGAGAGATTACAGAGATGTATG	281
Db	206	CGCGTGCAAAATCGATCCCGAAGAGGAAGCTTATGTGCCAGAGGATTACGATGATGTG	265
QY	282	GGGTGAGATTTCAGATCATGATCATCTCTCTGAGCATCCAAATTTGTTTAGGATCAAAGG	341
Db	266	GAGGAGAGATTTCAGATCATGACCAATTTGTGCGAGCATCCAAACGTTGTCCAGATCAAAGG	325
QY	342	GACTTATGAAGATTCCGGTGTGTTGTTCTATTTGTTATGGAGGTTTGTGAAGGTCGTGAGCT	401
Db	326	CAGGTACAGAGANTCCGTGTTCTGTCGACCTTGTCTAGGAACACTATGTCCGCGCGGGAGCT	385
QY	402	TTTTGATCGGATTGTTTCTTAAAGTCTATTTTAGTGAGCGTGAAGCTGTCTAAGCTTATTAA	461
Db	386	TTTCACACGAGTCAATTCAGAAAGGGCGATTAACGCGAGAGAGAGGCTGCCAAGTTGATAAA	445
QY	462	GACGATCTCTGGTGTGTTGAGGCTTGTCTATTCCTCTGTTGTTATGTCATAGAGATCTCAA	521
Db	446	GACCATTTGTGGGGTGGTGGAGGCGTGCCACTCTCTTTGGGGTCATGCATAGGAGATCTCAA	505
QY	522	AOCTGAGAAATTTCTTTGTTGTAGTCTCTTAAAGATGATGCTAAGCTTAAGGCTACCGATTT	581
Db	506	GCCTGAGAAATTTCTTTGTTGATACCCCTGGCGAAGATGCCAGATGAAGCCACCGATTT	565
QY	582	TGGTTTGCTGTCTCTATAGCCAGACACATATTTATATGACGTAGTTCGGAAGTCGGTA	641
Db	566	TGGCTCTCTGTCTATTCTACAAGCCAGACAGACGCTTTCATGATGTAGTAGGAAGTCCCTA	625
QY	642	CTATGTTGCCACACAGAGTGTCTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGAGTGC	701
Db	626	CTATGTTGCCCCAGAGGTGTGTGCCACCAATATGGACCTGAAGTGGACGTATGGAGTGC	685
QY	702	TGGTGTATCTCTACATTTTACTCAGCGGTGTCTCCCTTCTGGGCACAGACTGAGTC	761
Db	686	TGGTGTATCTCTATACATCTTACTGAGTGGGGTGCCACCTTCTCGGCTGAAACCCGAAGC	745
QY	762	TGGAATCTTTACACAGATATTGCAAGGGAAGTTAGATTCAAAATCTCACCCGTGGCCTAC	821
Db	746	AGGAATTTACACAGATTTTAAATGGAGATCTTGATTTGTTTCTGAAACGTGGCCAAAG	805
QY	822	TATCTCAGAAAGCTGTAAAGATTGATCTATAAAATGCTGAAAGGAGCCCCAAGAAACG	881
Db	806	TATCTCAGAAATGCTTAAGAAATGCTTAAACAGATGTGGATAGGAGACCTTAAGAAAAG	865
QY	882	CATTTCTGCTCATGAAGCCTTGTGCACCCATGGATTGTGATGAAACAAGACGACCCAGA	941
Db	866	AAATTTCTGCTCATGAAGTTTATGTPAACCTTGGGTTGTGATG---ACATTCGACCTGA	922
QY	942	CAAGCCTCTTGATCCAGCAGTCTTATCTCTGCTCTAAAGCAGTTTTTCTCAAAATGAATTAAGT	1001
Db	923	CBAACCTCTGGACTCTGCTGTTTGTGACACGCTTAAAGCATTTTCTCAGCAATGAATAAAT	982
QY	1002	TAAGAAAATGGCATTTACGGGTAAATTGCTGAGAGACTTTTCAGAGAAAGAAATTTGAGGTCT	1061
Db	983	TAAGAAAGATGGCATTTACGGGTCTATAGCAGAGAGGCTTTTCAGAGAAAGAAATAGGTGGATT	1042
QY	1062	GAAGGAATTTTCAAGATCATAGACACACAGCAAAACAGCGGAACGATTACTTTTGAAGAGCT	1121
Db	1043	GAAGAGATTTGTTTAAATGATTTGACACAGACAAATAGTGGGACATAACTTTTGGGAACT	1102
QY	1122	CAAAAGCGGTTTGAAGAGAGTCCGATCTGAACTGATGGAATCGAAATCTAAGTCTCTCAT	1181
Db	1103	GAAGGAGGGGTTCAAAAGTGTGGGCTCTAACTCATGGAATCTTGAAATCTCAAAATCACCTTAT	1162
QY	1182	GGATCGGCTGATATCGACAAACAGTGTGTAATAGACTACGGAGAAATCTTAGCAGCAAC	1241
Db	1163	GGAAAGCGGCTGATATAGACAAACATGGATCAATAGACTATGCTGAATTTCTTGCTGCTAC	1222
QY	1242	CTTACACATGAACAAGATGGAGAGAGAGAGATTTCTGGTGGCTGCATTTTTCGCACTTTGA	1301



2y 1126 GCGGTTTGAAGAGAGTCGGATCTGAAGTGAATGAAGATCAAGATCAAGTCTCTCATGGAT 1185  
Db 1077 GAGGTTTGAAGAGAGTCGGATCTGAAGTGAATGAAGATCAAGATCAAGTCTCTCATGGAT 1136  
2y 1186 GCGGCTGATATCGAACAAGTGGTACAAATAGACTACGAGAAATCCCTAGCAGCAACTTA 1245  
Db 1137 GCGGAGACATTGACAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAAT 1196  
2y 1246 CACATGAACAAGATGAGAGAGAGAGATCTGGTGGTGCATTTTCGAGCTTTGACAAA 1305  
Db 1197 CATTGAAACAATTCGAAAGGAGAGAAATCTGTTATCAGCCCTCTCTTATTTTGACAAA 1256  
2y 1306 GACGAAGCGGTTATATCACCATGATGAGCTTCAGTCAGCTGCACAGAGTTTGGTCTA 1365  
Db 1257 GATGGTAGTGATATCAATCAATTCGAAAGCTTCAGCAAGCTTCGAAAGAAATTTGGTCTT 1316  
2y 1366 TGTGATACACCTCTCGGACCATGATCAAGAGATATGATCTTGAGATGAGAGAGATC 1425  
Db 1317 AGCAGCTCAATCTTGATGAAATTTAAAGATATGATCAAGATATGATGAGAGAT 1376  
2y 1426 GATTCTCGAGTTTACAGCAATGATGAGAGAG--AGATGAGTTGGAGAGCAGA 1482  
Db 1377 GACTATAGGAATTTCTGCAATGATGAGAGAGAGCAGGTGAGAGCGTTGGAGAGG 1436  
2y 1483 ACCATGATGAAGAACTTGAACCTTCAACATCTGATGCTTTTGGAGTTGATGTTGAAAAA 1542  
Db 1437 ACCATAAGAAACAATTTGAATTTAGGAGAGCAGTACGAGTCTGACAGAGTG--AAGAAA 1494  
2y 1543 TGTGATGAGTACTGATCATCTTCTGCAATTTCTGTTTCTTTTCTCTTTAAATTCGTTT 1602  
Db 1495 TCTTATGAACCAACCAATTAATCCGAAACAGAGTTCGAGTGTATCTTCTAATTTCTTGTG 1554  
2y 1603 ATAT 1606  
Db 1555 ACAT 1558

RESULT 7  
AX077706 1768 bp DNA linear PAT 22-FEB-2001  
LOCUS AX077706  
DEFINITION Sequence 13 from Patent WO0107592.  
ACCESSION AX077706  
VERSION AX077706.1 GI:13122081  
KEYWORDS  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE 1 (bases 1 to 1768)  
AUTHORS Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.  
TITLE Herbicide resistant plants and methods for the production thereof  
JOURNAL Patent: WO 0107592-A 13 01-FEB-2001;  
ZENECA LIMITED (GB)  
FEATURES  
source Location/Qualifiers  
1..1768  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
BASE COUNT 511 a 325 c 464 g 468 t  
ORIGIN

Query Match 43.3%; Score 756.4; DB 6; Length 1768;  
Best Local Similarity 70.8%; Pred.No.3.4e-153;  
Matches 1009; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

2y 106 GTTCTACCATATCAACACCCAGGATTAAGATCATTAACCTTCGGGAAAAAAGCTAGGC 165  
Db 195 GTTCTCCGAGCGCAGCAGCAACATCCGAGGTGTACAGAGTTGGCGGAGGCTCGGG 254  
2y 166 CAAGCCCAATTTGAACAACCTATCTCTGCACAGAGAAATCAACCTCCGCTAATACGC 225

Db 255 CAGGCCAATTCGGGACCACCTTCGAGTGCAAGCCGCTGCGAGTGGTGGGAAGTTTCGGC 314  
2y 226 TGAATTCGATCCGAAGCAAAAGCTCGTGTGCGAGATTTACGAATGTATGGCCT 285  
Db 315 TGAAGTCGATTCGAAGCGGAAGCTGCTGTGCAAGAGAGACTACGAGGACGTGTGCGCG 374  
2y 286 GAGATTGAGATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAAAGGATC 345  
Db 375 GAGATTGAGATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAAAGGATC 434  
2y 346 TATGAAGATTCGGTGTGTTGTTCAATTTGTTATGAGAGTTTGTGAAGTGTGAGCTTTT 405  
Db 435 TACGAGGATTCACGCGCGTGCACCTGGTCAATGGAGTTGTCGAGGTTGAGAGTTGTT 494  
2y 406 GATCGGATTTGTTCTTAAAGGTCAATTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACG 465  
Db 495 GACAGGATCTGACAGAGAGGACACTACAGCGAGAGACAGCGCGGAGGTTGATAAAGACG 554  
2y 466 ATCTGTGTGTTGTTGAGGCTGTGCTCTCTCTGAGTCTCTCTCTGAGTCTGAGTCTG 525  
Db 555 ATCTGTGTGTTGTTGAGGCTGTGCTCTCTCTGAGTCTCTCTCTGAGTCTGAGTCTG 614  
2y 526 GAGATTTCTGTTGTTGATAGTCTCTTAAAGATGATGCTAAAGCTTAAAGCTACCGATTTTGGT 585  
Db 615 GAGATTTCTGTTGTTGATAGTCTCTTAAAGATGATGCTAAAGCTTAAAGCTACCGATTTTGGC 674  
2y 586 TTGCTGTCTCTTAAAGCCAGGACAATATTTATAGAGTGTGAGTGTGAGTCCGTACTAT 645  
Db 675 TTGCTGTCTCTTAAAGCCAGGACAATATTTATAGAGTGTGAGTGTGAGTCCGTACTAT 734  
2y 646 GTTGACACAGAGGTCCTTAAAGAAATGTTATGAGCTCAAAATAGATGTGCGAGTGTGGT 705  
Db 735 GTTGACACAGAGGTCCTTAAAGAAATGTTATGAGCTCAAAATAGATGTGCGAGTGTGGT 794  
2y 706 GTTATCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTGAGGAGAGACTGAGTCTGGA 765  
Db 795 GTTATCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTGAGGAGAGACTGAGTCTGGA 854  
2y 766 ATCTTTAGACAGATTTGCAAGGAGTGTAGATTTCAAAATCTGACCGTGGCTTACTATC 825  
Db 855 ATCTTTAGACAGATTTGCAAGGAGTGTAGATTTCAAAATCTGACCGTGGCTTACTATC 914  
2y 826 TCAGAGAGTGTCTTAAAGATTTGATCTTAAAGATGCTCGAAAGAGGCCCAAGAAACGCA 885  
Db 915 TCAGAGAGTGTCTTAAAGATTTGATCTTAAAGATGCTCGAAAGAGGCCCAAGAAACGCA 974  
2y 886 TCTGCTCATGAAGCCTTGTGTCACCCATGATGTCGATGACAGCAGCAGCAGACAAG 945  
Db 975 ACAGCACATGAAGTACTCCGCCACCCATGAGTGTGATGACAAACATTTGACACCTGATAA 1034  
2y 946 CTCTTTGATCCAGCAGTCTTATCTGCTTAAAGCAGTCTTCTCAATGAATTAAGATTAAG 1005  
Db 1035 CTCTTTGATCCAGCAGTCTTATCTGCTTAAAGCAGTCTTCTCAATGAATTAAGATTAAG 1094  
2y 1006 AAAATGGCATTACGGGTAAATGCTGAGAGACTTTTCAGAGGAGAAATTTGAGGCTCTGAAG 1065  
Db 1095 AAGATGGCATTACGGGTAAATGCTGAGAGGCTTATCTGAGAGGAAATTTGAGGCTCTGAAG 1154  
2y 1066 GAATTTCTTCAAGATGATGACACACAGCAACAGCGGAGCAATTTACTTTTGAAGAGCTCAAA 1125  
Db 1155 GAGTTATTCAGATGATGACACACAGCAACAGCGGAGCAATTTACTTTGATGAGTATAAA 1214  
2y 1126 GCGGTTTGAAGAGAGTCCGATCTGAATGATGAGAAATCAGAAATCAAGTCTCTCATGGAT 1185  
Db 1215 GATGGTTTGAAGAGAGTCCGATCTGAATGATGAGAAATCAGAAATCAAGGATCTTATGGAT 1274  
2y 1186 GCGGCTGATATCGAACAAGTGTGATCAATAGACTACGAGAAATTCCTAGCAGCAACCTTA 1245  
Db 1275 GCTCGGATATTCGATTAAGAGTGGGCAATTTGATGATGATTTCAATCTGCTCCACTGTT 1334  
2y 1246 CACATGAACAAGATGAGAGAGAGGAGATTTCTGTTGGTGTGATTTTCGAGTCTTGACAAA 1305  
Db 1335 CATTTAAATAAGCTGAGAGAGAGGAGAAACCTAGTGTGCGGCTTCTCTCTTATTTGACAAA 1394

QY 1306 GACGGAAGCGGTATATACCATCGATGAGCTTCAGTCAGCTTCCACAGAGTTTGCTCTA 1365  
 Db 1395 GATGGCAGTGGTTACATAACCTTGTATGAGATACAAACGCTTGTAGGACITTTGTTTA 1454  
 QY 1366 TGTGATACCTCTCGAGACATGATCAGAGATTTGATCTTGACATGACGGAGATC 1425  
 Db 1455 GATGATATCCATATTGACGATGATCAAGGAAATTCATCAAGATACCGATGGGCAATA 1514  
 QY 1426 GATTCTCGAGCTTTACAGCAATGATGAGGAAGGAGATGAGTTGGGGAAGACAGAAC 1485  
 Db 1515 GATTATGGGGAATTTGCTGCCATGATGAGGAAGGCAATGAGGAAATGGAGGCGAACT 1574  
 QY 1486 ATGATCAAGAACTTCAACTTCACATTCCTGATGCTTTTGGAGTTGATGG 1535  
 Db 1575 ATGAGAAAACACTAAATTTAAGAGATCTCTTGGATAGTAGCAATGG 1624

RESULT 8  
 SOYCADPK 1768 bp mRNA linear PLN 23-MAY-1996  
 LOCUS Glycine max calcium dependent protein kinase mRNA.  
 DEFINITION M64987  
 ACCESSION M64987.1 GI:169930  
 VERSION calcium/calmodulin-dependent protein kinase.  
 KEYWORDS Glycine max cDNA to mRNA.  
 SOURCE Glycine max  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 REFERENCE 1 (bases 1 to 1768)  
 AUTHORS Harper,J.F., Suesman,M.R., Schaller,G.E., Putnam-Evans,C., Charbonneau,H. and Harmon,A.C.  
 TITLE A calcium-dependent protein kinase with a regulatory domain similar to calmodulin  
 JOURNAL Science 252 (5008), 951-954 (1991)  
 MEDLINE 91240279  
 PUBMED 1852075

FEATURES  
 source  
 1..1768  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /germline  
 1..131  
 /note="putative"  
 38..76  
 /function="unknown"  
 /note="putative"  
 /codon\_start=1  
 /product="unknown protein"  
 /protein\_id="AAB00806.1"  
 /db\_xref="GI:1332393"  
 /translation="MASSKREENTN"  
 132..1658  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="AAB00806.1"  
 /db\_xref="GI:169931"  
 /translation="MAAKSSSSSTTNVVTAKAAYLPORITQIREVVEGKLGQGO  
 FGTPECTRRASGCKPKKIPKRLCKEDYEDVWEICIMHLSHANVVRLEGTY  
 EDSATVHLVMLCEGGLFRIKQGHYSERQARLIKTIWEVACHSLGVHMRDLK  
 PENFLFDIDDAKLKATDGLSVFYKPSGFCVGVYVAPVLSKLYGPSVDYV  
 SAGVILYLLSGSPFWASEPFIQILLGLKLPFSEFPWPSISDSKDLIRKMLDQV  
 PKRLTAHEVHVRHVIWDDNIAPDKPLDSAVLSRLKQFSAWMLKXKMLRVIAERLE  
 BEIGGLKELFMIDTNSGITFDLKGDLKRVSELSMESEIKDLMADIDKSGTID  
 YGEFTAAVHVKLEENELVSAFSPYDKGSGYITLDEIQQACKDFGLDIDHDDMI  
 KEIDQNDQIDYGEFAFMWRKNGGIGRTMKTNLRLDALGLVDSNGSNQVIEGYK  
 "

BASE COUNT 511 a 325 c 464 g 468 t  
 ORIGIN  
 \*Query Match 43.3%; Score 756.4; DB 8; Length 1768;

Best Local Similarity 70.6%; Pred. No. 3.4e-153;  
 Matches 1009; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

QY 106 GTTCTACCATATCAACACACACGATTAAAGAGATCATTAACCTTCTGGGAAAAAAGCTAGGC 165  
 Db 195 GTTCTCCCGCAGCGACGCAACATCCGTGAGGTGTACGAGTTGGCGGAGCTCGGG 254  
 QY 166 CAAAGCAATTTGGAAACAACTTCTCTGCAACAGAGAAATCAACCTCCGCTAAATACGC 225  
 Db 255 CAGGGCAATTCGGGACCACTTCGAGTGCACGCGCGCTGCGAGTGGTGGAAAGTTTCGG 314  
 QY 226 TGCAAATCGATCCCGAAGCAAGCTCGTGTGCGGAGGATTACGAAGATGTATGGCGT 285  
 Db 315 TCGAAGTCGATTCGGAAGGGAAGCTCTGTGCAAGGAGGACTACGAGACGCTGTGGCG 374  
 QY 286 GAGATTCAAGATCATGCTATCTCTGAGCATCCAAATGTTGTTAGGATCAAGGAGCT 345  
 Db 375 GAGATTCAAGATAATGCACCACTTGTTCGGAAACACGCCAACCTTGTCCGCATCGAAGGAG 434  
 QY 346 TATGAAGATTCCGTGTTTGTTCATATTGTTATGAGGCTTTGTGAAGGTGGTGAGCTTTT 405  
 Db 435 TACGAGATTCCACGCGCTGCACCTGCTCATGGAGTTGTGCGAGGCTGGAGAGTTGTTT 494  
 QY 406 GATCGGATTTCTTAAAGGTCAATTTTAGTGAAGCTGAAGCTGTCAAGCTTATTAAGAG 465  
 Db 495 GACAGATCTGTCAGAGAGGACACTACACGAGAGACAGCGCGGAGGTTTGAATAAGAG 554  
 QY 466 ATTCTTGGTGTGTTGAGGCTGTCTCTCTGCTGTTATGATAGAGATCTCAAAACCT 525  
 Db 555 ATTGTTGAGTTTGTGAGGCTGTCTCTCTGCTGTTATGATAGAGATCTCAAAACCT 614  
 QY 526 GAGATTTCTTGTGATGCTTAAAGATGATCTAAGCTTAAAGCTAAGCTACCGATTGTTGT 585  
 Db 615 GAGATTTCTTGTGATGCTTAAAGATGATCTAAGCTTAAAGCTAAGCTACCGATTGTTGT 674  
 QY 586 TTCTCTGCTTCTTATAAGCAGGACAAATATTATATCATGCTAGTTGGAAGTCCGCTACT 645  
 Db 675 TTGTCGTGTTTTCAGACCTGCTGTAATCCCTTTTGTGATGTTGTCGGGACCCACTAT 734  
 QY 646 GTTGACACAGAGGCTCTAAAGAAATTTATGAGCTGAATAGATGTGTGGAGTGTGCTGT 705  
 Db 735 GTCGACACAGAGGCTCTTTCGCAAGCTCTATGAGCTGAATAGATGTGTGGAGTGTGCTGT 794  
 QY 706 GTTATCCTCTACATTTTACTCAGCGGTGTTCTCCCTCTTGGGACAGAGCTGAGTCTGGA 765  
 Db 795 GTTATCTCTACATCTTATTAAAGTGGGTGCCACCAATTTTGGGCGGAATCTGAACCGGG 854  
 QY 766 ATCTTTAGACATATTTCGAGGGAAGTTAGATTTCAATCTGACCGCTGCGCTACTATC 825  
 Db 855 ATCTTCGACAGATTTTACTAGGAAACTTGAATTTTCTGAGCTTGGCCTAGCATT 914  
 QY 826 TCAGAGAGCTGCTAAAGATTTGATCTTATAAATGCTCGAAAGAGGCGCCCAAGAACGCA 885  
 Db 915 TCAGACAGTGTCCAAGGATCTAATTCGGAAATGCTTGTATCAAAATCCAAATAACAGGCT 974  
 QY 886 TCTGCTCTGAAGCCTTGTGTGCCCATGGAATGTCATGATGAACAGCAGCACCAGACAG 945  
 Db 975 ACAGCACATGAAGTACTCGGCGACCCATGGATTGTTGATGACAACTTGCACCTGTATAA 1034  
 QY 946 CCTCTTGTATCCAGCAGCTTCTATCTCGTCTAAAGCAGTTTTCTCAAAATGAATAAGATT 1005  
 Db 1035 CCTCTTGTATCTCGAGTTTATCACTGTAACAATTTCTGTCATGAATAAATGAA 1094  
 QY 1006 AAATGGCATACGGGTAAATGCTGAGAGCTTTTCAGAGGAGAAATGGAGCTCTGAAG 1065  
 Db 1095 AAGATGGCATTCGGTGTATTGCTGAGAGGCTATCTGAAGAGAAATTTGGTGAAGTAAA 1154  
 QY 1066 GAATTTCTCAAGATGATAGACACACAGCAACAGCGGCAACGATTACTTTTGAAGAGCTCAA 1125  
 Db 1155 GAGTATTCAAGATGATTGACACACACCAACAGTGAACCACTAACGTTTGTATGAGTAAA 1214  
 QY 1126 GCGGTTTGAAGAGAGTGGATCTGAACCTGATGGAATCAGAAATCAAGTCTCTCTGAT 1185

```

Db 1215 GATGTTTAAAGCAGTAGTCTGAACTTATGAGTCTGAAATCAAGGATCTTATGGAT 1274
QY 1186 GCGGTGATATCGACACAGTGGTACAAATAGACTACGAGAAATCTTACGAGCAACTTA 1245
Db 1275 GCTGGGATATTTGATAAAGTGGGACAAATGATTATGTTGAATCAATCTGCTGCACTGTT 1334
QY 1246 CACATGACAGATGGAGAGAGAGAGATTTCTGGTGGCTGCTATTTTCGGACTTTGACAAA 1305
Db 1335 CATTTAAATAAGCTGGAGAGAGAGAAACCTAGTGTGGGCTTCTCTATTTTGACAAA 1394
QY 1306 GACGGAAGCGGTTATATCACCATCATGAGCTTCAGTCTGAGCTTGCACAGAGATTTGGTCTA 1365
Db 1395 GATGGAGTGGTTTACATAACCTTGTATGAGATACAAACAGCTTGTAAAGCACTTTGGTTTA 1454
QY 1366 TGTGATACACCTCTGGAACATGATCAAGAGATTTGATCTGCAATGATGAGGGAAGATC 1425
Db 1455 GATGATATCCATATTTGACACATGATCAAGGAAATTTGATCAAGATACATGATGGCAATA 1514
QY 1426 GATTTCTCGAGTTTACAGCAATGATGAGGAAGGAGATGGAGTTGGGAGAGCAGAAC 1485
Db 1515 GATTATGGGGAATTTCTGCTCCATGATGAGAAAGGCAATGGAGGAATTTGGAAGCGCACT 1574
QY 1486 ATGATGAAGAACTTGAACTTCAACATTTGCTGATGCTTTTGGAGTTGATGG 1535
Db 1575 ATGAGAAAAACACTAAATTTAAGAGATGCTCTTGGATTAGTAGACAATGG 1624

RESULT 9
ATACDPK9 1693 bp mRNA linear PLN 10-SEP-2001
LOCUS Arabidopsis thaliana calcium dependent protein kinase mRNA,
DEFINITION complete cds.
ACCESSION U20388
VERSION U20388.1 GI:836937
KEYWORDS calcium dependent protein kinase.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1693)
Hong Y., Takano M., Liu C.M., Gasch A., Chye M.L. and Chua N.H.
Expression of three members of the calcium-dependent protein kinase
Gene family in Arabidopsis thaliana (1996)
Plant Mol. Biol. 30 (6), 1259-1275
96311013
MEDLINE PUBMED
8704134
REFERENCE 2 (bases 1 to 1693)
Hong Y.
Direct Submission
Submitted (27-JAN-1995)
Yan Hong, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore, Republic of Singapore, 0511
Location/Qualifiers
Location 1..1693
organism="Arabidopsis thaliana"
strain="Columbia"
db_xref="taxon:3702"
38..1510
/codon_start=1
/product="calcium-dependent protein kinase"
/protein_id="AAA67653.1"
/db_xref="GI:836938"
/translation="MANKERTRWLPYKTKNVEDNVFLGVLGQGFQFTFLCTHKOT
GQKLAKSPKRLKLCQEDYDVLREIQMHLSYPNVVRIESAYEDTKNHLVMEI
CEGEULFDRIYKXGHSREAAKJIKTVGVVEACHSLGVHRDLKPNFLPSSDED
ASLSTDFGLSVFTPEAFSELVYAVPEVLHKHYPEDCVMSAGVLIYLLCG
FPFWAESEIGKILQKLEFENPWSISASAKLIKMLNPNPKRLTAHVLIC
HPWVDDKVPADPLCAVVRKPSAMNKLKQALRVIAERLSEIEGIGKELFKM
LDTDKSTITFEELKDSMRVSGELSEBIQELLRAADVDESGTIDYGEFLAAIHLN
KLREENLVAAPFPKDSAGYTIIELOQANKERGINSLNDEMIKIDIDNDQDQID
YGEFVAMWRKNGTGGIGRITVRNSLNFSTLIPDESNNV"
1693
polyA_site

```

```

BASE COUNT 516 a 296 c 395 g 486 t
ORIGIN
Query Match 42.8%; Score 744.2; DB 8; Length 1693;
Best Local Similarity 70.0%; Pred. No. 1.5e-150;
Matches 1001; Conservative 0; Mismatches 428; Indels 0; Gaps 0;
QY 106 GTTCTACCATATCAAAACACACAGGATTAAGAGATCATTTACCTCTCGGAAAAAAGCTAGGC 165
Db 65 GTTCTTCTTACAGACCAAAAGCTTGAAGACAAATTTACTTTCTTGGTCAAGTCCITGGA 124
QY 166 CAAGCCCAATTTGGAACAACTATCTCTGACAGAGAAATCAACCTCCGCTAATTAGGCC 225
Db 125 CAAGCCCAATTTGGAACCACTTTCTCTGTACCCATAAAACAGACAGGTCAAAAGCTTGC 184
QY 226 TGCRAATCGATCCGAGAGCAAGCTCGTGTGCGAGGATTACGAAGATGTATGGCGT 285
Db 185 TGCRAATCCATACCCAAAGGAGCTCTTTGTCAAGAGATTTACGACGAGCTTCTGAGA 244
QY 286 GAGATTCAGATCATGCATCATCTCTGAGCATCCAAATTTGTTAGGATCAAAAGGACT 345
Db 245 GAGATCCAGATAATGCATCACTTGTCTGAATACCCCAACGTTGTCCGTATAGAGAGTGG 304
QY 346 TATGAGATTCGGTGTGTTTTCATATTTATGAGAGTTTGTGAAGTGTGAGCTTTT 405
Db 305 TACGAGGACACCAAAACGTCATCTTGTGATGGAGCTTTGTGAGAGAGTGTGCTTTT 364
QY 406 GATCGGATTTGTTCTTAAAGGTCATTTAGTGAGCGTGAAGCTGTCAAGCTTTATTAAGCG 465
Db 365 GATAGATTTGGAAGAGAGGTCATTTACAGTGAAAGAGAGCTGTAAGCTTATCAAGACC 424
QY 466 ATCTTGGTGTGTTGAGGCTGTGCTCTCTTGGTGTATGATAGAGATCTCAACCT 525
Db 425 ATTTGTTGGGTTGTTGAGCGGTGTCACCTCTCTTGGTGTGTTGATAGAGATCTTAAGCT 484
QY 526 GAGATTTCTGTTGATAGTCTTAAAGATGATGCTAAAGATGATGCTAAAGGCTACCGATTTTGGT 585
Db 485 GAGATTTCTGTTTCTTCTCTGATGAAGATGCTTCTTAAATCTTACTGACTTTGGC 544
QY 586 TTGCTGTCTTTCTAAGCCAGGACAAATTTATATGACGTAGTTGGAAGTCCGCTACTAT 645
Db 545 CTCTCTGTTTCTGACACACAGAGAGACATTTTCGGAACCTCGTTGGTAGTGTCTACTAT 604
QY 646 GTTGCCACAGAGTGTCTAAAGAAATGTTATGACCTGAAATAGATGTGTGGAGTGTCTGGT 705
Db 605 GTGGCACCTGAGTTTACATPAAGCAATTTATGCTCTGATGTGACATGAGTGTCTGGA 664
QY 706 GTTATCCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCTGGGACAGACTGAGTCTGGA 765
Db 665 GTTATCCTCTACATTTCTTATGTGTTTCTCTCTCTTTTGGGCTGAGAGTGAATAGGC 724
QY 766 ATCTTTAGACAGATATGCAAGGAGTGTAGATTTCAATCTGACCCGTGGCTACTATC 825
Db 725 ATCTTCAGGAAGATTTTACAGGAAAGTTGGAGTTTGAGATCAATCTCTTGGCTAGCATT 784
QY 826 TCAGAAAGCTGTAAAGATTTGATCTATATAAATGCTCGAAAGAGGCCCAAGAACGCAATT 885
Db 785 TCAGAGAGTGCCAAAGATCTTATAAGAAAAATGCTTGAAGCAATCTCTAAAAAGAGGCTA 844
QY 886 TCTGCTCATGAACCTTTGTCTACCCATGGATTGTGATGAAACAGACAGCAGACACAAG 945
Db 845 ACTGCTCATCAAGTGTGTGTCTCATCGTGGATTGATGATGATGATGATGATGATGATGAT 904
QY 946 CCTCTTGATCCAGCAGTCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1005
Db 905 CCTTTGAGCTGCGGGTGTGTCGCCCTGGAAGAGTTCTCTGCAATGAACAACTTAAG 964
QY 1006 AAATGSCATTACGGGTAAATGCTGTGAGACATTTTACAGGAGAAATTTGGAGCTGAGG 1065
Db 965 AAGATGSCATTACGGGTAAATGCTGTGAGAGACATCTCTGAGGAGAAATTTGGTGTCTCAA 1024
QY 1066 GAATTTGTTCAAGATGATAGACACAGCAACAGCGGAACGATTACTTTTGAAGAGCTCAA 1125

```

```

Db 1025 GAACCTGTTCAAAATGATACACACAGATAAAAGTGGGACTATCACTGTTGAAGAGTTAAAAA 1084
Qy 1126 GCGGGTTTGAAGAGAGTGGGATCTGAATGATGGAATCAGAAATCAAGTCTCTCATGGAT 1185
Db 1085 GATAGATAGAGAGTGGGTCAGAGCTTATGGAATCAGAGATCCAGAACTCTTGGCT 1144
Qy 1186 GCGGCTGATATCGAACACAGTGGTCAATATAGACTACGAGAAATTCCTPAGCAGAACTTTA 1245
Db 1145 GCGGCTGATGTTGATGAGAGTGGAAATTCAGTATGAGAGTCTTCTAGCTGCAACAATC 1204
Qy 1246 CACATGAACAAGATGAGAGAGAGAGATTCCTGGTGGCTGCATTTTCGGACTTTGACAAA 1305
Db 1205 CACTTGAACAACCTGGAGAGAGAGAGATCTAGTAGCTGCAATCTCTTCTTTGATAG 1264
Qy 1306 GACGGAAGCGGTTATATACCAATCGATGAGCTTCAGTCAGCTTCCACAGAGTTTGGTCTA 1365
Db 1265 GATGCAAGTGGTTATCATCACTATCGAAGAGCTTCAACAGGAGATGGAAGGAGTTGGTATA 1324
Qy 1366 TGTGATACACCTCTGGACGACATGATCAAGGAGATTTGATCTTGACAAATGACGGGAAGATC 1425
Db 1325 AACGATTTAAATCTTGATGAATGATCAAGACATTTGATCAAGATATGATGACAAATA 1384
Qy 1426 GATTTCTGGAGTTTACAGCAATGATGAGGAAGAGAGATGAGTTGGGAGAGCAAGAAC 1485
Db 1385 GACTATGGAGAAATTTGTGCAATGATGAGGAAGAGAAATGSCACTGGAGGAGGATTTGGT 1444
Qy 1486 ATGATGAAGAATCTGAACCTTCAACATTCGATGCTGATGCTTTTGGAGTTGATG 1534
Db 1445 CGGAGAACTATGAGGAACCTCTCAACITTTGGAACTACTCTTCTCTGATG 1493

RESULT 10
ATU1835
LOCUS
DEFINITION
  Arabidopsis thaliana 2036 bp mRNA linear PLN 23-AUG-2001
  6 (CPK6) mRNA, complete cds.
ACCESSION
  U31835
VERSION
  U31835.1 GI:1399274
KEYWORDS
  Arabidopsis thaliana.
SOURCE
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 2036)
  Hrabak E.M., Dickmann, L.J., Satterlee J.S. and Sussman, M.R.
  Characterization of eight new members of the calmodulin-like domain
  protein kinase gene family from Arabidopsis thaliana
  Plant Mol. Biol. 31 (2), 405-412 (1996)
  2 (bases 1 to 2036)
  Hrabak, E.M.
  Direct Submission
  Submitted (18-JUL-1995) Eberle Hrabak, Horticulture, University of
  Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
  Location/Qualifiers
    1..2036
      /organism="Arabidopsis thaliana"
      /strain="Columbia"
      /db_xref="taxon:3702"
      /chromosome="2"
    1..2036
      /gene="CPK6"
      /note="calcium-dependent protein kinase"
      /codon_start=1
      /product="calmodulin-domain protein kinase CDPK isoform 6"
      /protein_id="AA03246.1"
      /db_xref="GI:1399275"
      /translation="MGNSCRGSPKDIYEGNHSRPENSKSTTTTSSVHSHTDQDF

gene
CDS

```

```

SKONTNPALVTPVKEPIIMRNVDNQSYVYVGHKTNIRDLYTLTKSLGQGGTGYLTC
TDIATGYDYACKISKRKLISKEVDREBQIMHHLACHKNIVITIKGVEDPLVYH
IVLMLCAGBELFDRI THRGVYSERKAABLTIIIGVVEACHSLGVMHDLKPENFLIV
NKDDRLSKALDGLSVFEPKGOIFKDVVGSYVYVAPVLLKHYPGPRADVMTAGVILY
ILLSGVFPFAETQOQGFDAVLKGYIDPDTDPWVIDSASAKLIRKMLCSSPSELTA
HEVHKWPCVINGVAPDRALDPAFLSKLQFSAWMLKRWALKVIAESLSEETAGUR
AMPBAMTDNSGATITFDELKAGLRVYGTIDKTEIRDLMEAADVDNSGTIIDSEFIAA
TIHUNKLEBEHLVSAFOYFDKGSYITIDKEIQSCIEHGMTDVFLEDIKEVDQDN
DGRIDYEFVAMQKGNAGVGRMTKNSLNMRDV"
BASE COUNT      600 a 337 c 477 g 622 t
ORIGIN
Query Match      40.8%; Score 712.6; DB 8; Length 2036;
Best Local Similarity 68.1%; Pred. No. 1e-143;
Matches 991; Conservative 0; Mismatches 464; Indels 0; Gaps 0;
Qy 73  ACGAACCCAAACCTAGACGTCCTTCAACACAGCTTACCATATCAACACACCAATTA 132
Db 246  ATGCGCGTAACGTTGACAATCAATCTTACTATCTTCTGTCACAAGACTCCTAACTT 305
Qy 133  AGAGATCATTACCTTCTGGGAAAAGCTAGCCAGGCCAAATTTGGPACAACTATCTC 192
Db 306  CGTGATCTTTACAGTTGAGTCGTAACTTAGGACAGACAAATTCGGGACACGTAATTG 365
Qy 193  TGCACAGAGAAATCAACCTCCGCTAAATTAACCCCTGCAAAATCGATCCCGAAGCAAGCTC 352
Db 366  TGTACTCATATTTGCCACAGGTGTTGACTATGCTTGTGAAGTCTATATCCAGAGAGAAATTG 425
Qy 253  GTCTGTCGCGAGGATTACGAGATGATGGCGTGAGATTAGATCATGATCATCATCTCTCT 312
Db 426  ATATCTAAAGAGAGATGTTGAGGATGTTAGGAGGAGATTCAGATTATGCAATCTTAGCT 485
Qy 313  GAGCATCCAAATGTTGTTAGGATCAAGGGACTTATGAAGATTCGGTGTGTTGTTGTCATATT 372
Db 486  GGTCAACAAGAAATTTGTTACTATTAAGGAGCTTATGAGGATCTCTTGTATGTTCACATT 545
Qy 373  GTTATGAGAGTTTGAGAGGTGGTGGCTTTTGTGATCGGATGTTTCTTAAAGGTCAATTTT 432
Db 546  GTGATGGAGCTTTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 605
Qy 433  AGTGAGCTGAAGCTGTCTCAAGCTTATTAAGAGATTCCTTGGTGTGTTGTTGAGGCTTGTCAT 492
Db 606  AGCGAGAGAGAAAGCTGCTGAGTTGACCAAGATCATTTGCTGGTGTGTTGAGGCGTGCTCAT 665
Qy 493  TCTCTTGTGTTATGATAGATGATCTCAAACTCAGAAATTTCTTGTGTTGATAGTCTCTAA 552
Db 666  TCTCTTGTGTTATGATAGATGATTTAAAGCTCAGAAATTTCTTGTGTTGTTAATAGGAT 725
Qy 553  GATGATGCTAAGCTTAAGCTACCGATTTTGGTGTGCTGTCTTCTATATAGCCAGACAAA 612
Db 726  GATGATTTCTCTTAAAGGCCATTGATTTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 785
Qy 613  TATTTATATGAGCTAGTTGGAAGTCCGTAATCTGTTGACCAAGAGGTGCTTAAAGAAATGT 672
Db 786  ATATTCAAGGATGTTGTTGGAAGTCCATACATATGTTGCTCTGAGGTTCTCTTAAACAT 845
Qy 673  TATGGACCTGAATAGATGTGAGAGTCTGCTGTTTATCTCTACATTTTACTCAGGCT 732
Db 846  TATGGTCCAGAAAGCTGATGTGGACTGCTGGTGTATCTCTATATCTTACTAAGTGGT 905
Qy 733  GTTCTCTCTCTCTGCGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTTCGAAGGGAAG 792
Db 906  GTCCCGCTTTCTGGSCAGAAACACAGCAAGGAATATTGATGCTGTGTTGAAGGATAT 965
Qy 793  TTAGATTTCAATCTGACCCGTCCTACTATCTCAGAACTGCTGCTAAGATTTGATCTAT 852
Db 966  ATTGACTTTGATACAGACCCGTCCTGTCATATCCGACAGTGCCTAAGATCTGATCCGG 1025
Qy 853  AAAATGCTGAAAGAGCCCAAGAAACCGCAATTTCTGCTCATGAAGCTTTGTGTCAACCA 912
Db 1026  AAGATGTTATGCTCTAGTCTCTCTGAAGCTTTGAGTGTCTCATGAAGTCTTTCGCTCATCCA 1085
Qy 913  TGGATGTCGATGAACAGCAGCACCAAGCCTCTTGTATCCAGCAGTCTTATCTCTCT 972

```

[illegible]



QY 390 AGTGGTGGAGCTTTTGTATCGGATTTGTTCTTAAAGGTCATTTTAGTCAGCGTGAAGCTGT 449  
Db 1072 TGGGGGTGAGCTTTTCGATAGGATTAATCAACGGGGGCACTATACGGAAGAAAGAGCAGC 1131  
QY 450 CAAGCTTATTAAAGAGATCTTGTGGTGTGTTGTCAGCGCTTGTCAATCTCTCTGGTGTATGCA 509  
Db 1132 TGAGCTTACTAGGACTATTTGTGGGTGTAGAGCTTGTCAATCTCTCTGGTGTATGCA 1191  
QY 510 TAGAGATCTCAAACTGAGAAATTTCTTGTGTATGATCTCTTAAAGATGATGCTAAGCTTAA 569  
Db 1192 TCGTGATCTTAAAGCTGAAATTTTCTCTTTGTTGATCAGAGAGGATTCATCTCFAA 1251  
QY 570 GGTACCGATTTTGGTGTGCTGCTCTTATAAGCCAGGACAAATATTATATGACGTAGT 629  
Db 1252 AGCAATGTACTTTGGGTATCGATATCTTCAACAGCGGACGACAGATTTACTGATGTTGT 1311  
QY 630 TGAAGTCGTTACTATGTTGCAACGAGGTGCTAAAGAAATGTTATGACCTGAATAGA 689  
Db 1312 TGGCAGCCCATACTATGTCGACACGAGAGTTCTCGGAAAGGTTATGTCCTGAAGCTGA 1371  
QY 690 TGTGTGAGTGTGGTGTATCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTGGGC 749  
Db 1372 TGTTTGGAGTGTGGTGTATTTCTCTCACTATTTAAGTGGAGTACCTCTCTCTGGGC 1431  
QY 750 AGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAAACTGA 809  
Db 1432 TGAATATGACGAGGAATATTTGAACAGTCTCTGACGCTGATCTTGACTTCAAGTCAGA 1491  
QY 810 CCGTGGCTACTATCTCAGAGCTGCTTAAGATTTGATCTATATAAATGCTCGAAGGAG 869  
Db 1492 CCCATGCCAAGTATTTCAAGAGATGCAAAAGACTTGATGAGGAAATGCTGCTTCGAGA 1551  
QY 870 CCCCAAGAAACGCAATTTCTGCTCATGAAGCCTTGTGTACCCATCGATGTCGATGAACA 929  
Db 1552 TCCGAGNAGAGCTTTAACTGCACATGAAGTTTATGCCATCTTGGGTACAAGTTGATGG 1611  
QY 930 AGCAGACACAGAACGCTTGTATCAGCAGTCTTATCTGCTTAAAGCAGTTTCTCA 989  
Db 1612 TGTGGTCCCGATAAGCCTCTGGATTTCTGAGTCTGAGTGAATGAAGCAATTTTCTGC 1671  
QY 990 AATGAATAAGATTAAAGAAATGCAATAGCGGTAATGCTGAGAGACTTTTCAGAGGAAGA 1049  
Db 1672 AATGAACAACCTCAAGAAATGCTTTGAGAGTCAATGCTGAAAGCCTATCGAAGAGA 1731  
QY 1050 AATTGGAGTCTGAAGGAATGTTTCAAGATGATAGACACAGACACAGCGGAACGATTAC 1109  
Db 1732 AATTGCTGGTCTTAAAGAAATGTTCAAGATGATAGACACAGACCAATAGCGGTCAAATAAC 1791  
QY 1110 TTTTGAAGACTCAAAAGCGGTTTGAAGAGAGTCGGATCTGAACCTGATGGAATCAGAAAT 1169  
Db 1792 TTTTGAAGAGCTCAAAAGAGGTTTAAACGATTTGGCTCTAATCTGAAGGAGACCGAGAT 1851  
QY 1170 CAAGTCTCTCATGGATCGGCTGATATCGACAAACAGTGGTACAAATAGATACGGGAATT 1229  
Db 1852 CTATGATCTTATGAGGAGCTGACGCTGATGATAACAGTGGAACTAATGATTATGGTGAAT 1911  
QY 1230 CTTAGCAGCACTTACATGACAGATGAGAGAGAGGATTTCTGGTGGCTGATT 1289  
Db 1912 TATAGCTGCAACATTAATATGAACAAATTTGAAGACAGATCATCTTTTGTGCTTT 1971  
QY 1290 TTCGAGCTTTGACAAAGACGGAAGCGGTTATATCAACCATCGATGAGCTTCAGTCAAGCTTG 1349  
Db 1972 CTGTTACTTCCATAAAGATGAAAGTGGCTACATCACTCGGATGAGCTTCAACAGCTTG 2031  
QY 1350 CACAGAGTTTGGCTATGTATGATACCTCTGGACGACATGATCAAGAGATGATCTTCA 1409  
Db 2032 TGAAGAAATTTGGCATTTGGGATGTCGCGATGGAAGAAATGATCAGAGAGCTGACCAAGA 2091  
QY 1410 CAATCAGCGGAAGATTCGATTTCTCGGAGTTTACAGCAATGATGAGGAAGGAGATGGAGT 1469  
Db 2092 CAAATCAGCGGCGCATTTGCTACATGATGAGTTTGTGCTATGATGCAAAAGGAAATCCAGT 2151

QY 1470 TGGGAGAGCAGAACCATGATGAAGAACTTGAACCTTCAACATTTGCTGATGCTTTTGGAGT 1529  
Db 2152 GCTAGGTGGTGGCAAGAAAGGTCTAGAGCATATGTTTTCAGCAATTTGATTCAGAGACGACT 2211  
QY 1530 TGATGGTGAATAATCTGATGACTGACTCATCTTCCACATATTTCTGTTTTTTTCTC 1589  
Db 2212 AAAAATATAGAGAGCCCTTGAAGAGAAATTTTTCCTTAGTGTGTTGCTATATTTT 2271  
QY 1590 TTTAATTTCCGTTTATATTTT 1609  
Db 2272 CTTGGGAATTTTCTGTT 2291  
RESULT 13  
NTA344155 2437 bp mRNA linear PLN 03-NOV-2001  
LOCUS Nicotiana tabacum mRNA for calcium-dependent protein kinase 3  
DEFINITION (cdpk3 gene).  
ACCESSION AJ344155  
VERSION AJ344155.1 GI:16215470  
KEYWORDS calcium-dependent protein kinase; cdpk3 gene.  
SOURCE common tobacco.  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Nicotiana.  
REFERENCE  
1 Romeis, T., Ludwig, A.A., Martin, R. and Jones, J.D.  
Calcium-dependent protein kinases play an essential role in a plant  
defence response  
EMBO J. 20 (20), 5556-5567 (2001)  
JOURNAL 21481752  
MEDLINE 11597999  
PUBMED 11597999  
REFERENCE 2 (bases 1 to 2437)  
AUTHORS Romeis, T.  
DIRECT SUBMISSION  
TITLE Submitted (16-AUG-2001) Romeis T., The Sainsbury Laboratory, John  
Innes Centre, Norwich, Colney Lane, Norfolk, NR4 7UH, UNITED  
JOURNAL KINGDOM  
FEATURES  
source  
1..2437 Location/Qualifiers  
/organism="Nicotiana tabacum"  
/db\_xref="taxon:4097"  
374..2110  
/gene="cdpk3"  
374..2110  
/gene="cdpk3"  
/codon\_start=1  
/product="calcium-dependent protein kinase 3"  
/protein\_id="CAC82999.1"  
/translation="MGNTCVGPSISKNGIFQSVSAAMWRSRSPDDTASTNNGESARIE  
TPISVKPDPSPLPVQEPPEQMTVPKSEKEQPKPKPAEMKRVSSAGLRTDSV  
LOKGTNLKEFFSIGKLGQGFCTFKVEKATGKEYACKSIKRLITDDDEDVYR  
REVQIMHLAGHPHVISIKGAYDAVAVHVMFPCAGELFDRIIOGHVTERKAEL  
TRTVGVVEACHSLGWHRDLKPNFLFVQKEDSLKADFGLSIFFKPGDFTDVV  
GSPYVAPAEVRKRYGPEADVMSAGVITLLSGVPFFNAENQGGFEQVHLGDLPT  
SDPWSISDADKLRRMLVDRRLTAHEVLCHPWQVDGVAPDKPLDSAVLSNKK  
QFSAMNKLKMAIRVIAESBEIAGLKEMFKMIDTNSQGITFEELKDLKRFQSN  
LKESBIYDLMOAADVNSGTTDYGEFTAATLHMNKIERODHLFAAFQCFDKGSGYIT  
ADELQACEERFGIGVRMEEMIREADQDNDGRIDYNEFVAMVQKGNVGLGKKGLEH  
SFSIGFREAVKL"  
BASE COUNT 750 a 377 c 559 g 751 t  
ORIGIN

Query Match 39.9%; Score 696.8; DB 8; Length 2437;  
Best Local Similarity 65.1%; Pred. No. 2.6e-140;  
Matches 1028; Conservative 0; Mismatches 552; Indels 0; Gaps 0;

QY 30 AATTCGAGATCGAAGAGAACCAAAAAAACAATAATCGAGACGAGCCAAACCTAG 89  
Db 601 AAAAGAACAAACCAAAAAAGCCCAAAAGCCTCTGTAATGAAGAGGCTCTCAAGTGTG 660

QY 90 AGCTCCTTCAAAACAGTCTACCATATCAAAACACACAGATTAAAGAGATCAATTACCTTCT 149  
 Db 661 CTTAGGACAGATCTGTGTTTACAAAGAACTTGAACCTTTAAAGAGTCTTTTCAAGTAT 720  
 QY 150 GGGAAAGAGCTAGCCGAGGCAATTTGAAACACCTATCTCTGCACAGAGAAATCAAC 209  
 Db 721 AGGAAAGAAATTTAGACAGAGTCAATTTGGAACCTACATTTAAATGTGTGCAAAAGGCAAC 780  
 QY 210 CTCGCTAATTAAGCGCTTCAAAATCGATCCGAGAGGAAAGCTCGTGTGTCGGGAGATT 269  
 Db 781 AGGGAAGGAATATGCTTCAAAATCGATGCTTAAGAGGAAGTTGTTAAACAGATGATGAT 840  
 QY 270 CGAAGATGTATGGCTGAGATTCAGATCATGCTATCTCTGAGCATCCAAATGTTCT 329  
 Db 841 GGAAGATGTTAAGGGAAGTACAGATATCCACCATTTGGCAGGACATCTCTCATGTTAT 900  
 QY 330 TAGGATCAAGGAGACTTATGAGATTCGGTGTGTTGTTTCAATTTGTTATGAGAGTTTGA 389  
 Db 901 ATCGATAAAGGCTTATGAGGATGCTGTAGCTGTTCATGTTATGCGAGTTTGTGC 960  
 QY 390 AGTGTGAGCTTTTGTATCGGATGTTTCTAAAGGTCATTTAGTCAGGCTGAACCTGT 449  
 Db 961 TGGGGTGAGCTTTTCGATAGGATTAATCAACGGGGGACCTATACAGAAAGAAAGCAGC 1020  
 QY 450 CAAGCTTATTAAGACGATCTTGTGTTGTTGAGGCTGTCTCTCTCTGTTGTTATGA 509  
 Db 1021 TGAGCTTACTAGGACTATGTTGGAGTTGTAGAAGCTGTCTCTCTGTTGTTATGA 1080  
 QY 510 TAGAGATCTCAACCTGAGATTTCTTTTGTATAGCTTAAAGATGATGCTTAAGCTTAA 569  
 Db 1081 TGTGATCTTAAGCTGAAATTTCTCTTTGTTGATCAGAGGAGATTCATCTTCTCAA 1140  
 QY 570 GGCTACCGATTTGTTGTTGTTCTCTTATAAGCCAGGACAAATTTATATACCTGAT 629  
 Db 1141 AGCAATTGACTTTGGTGTATCGATATCTTCAACACGAGGACAGATTTACTGATGTT 1200  
 QY 630 TGAAGCTCGTACTATGTTGACACAGAGTGTCTAAAGAAATGTTATCGACTGAAATAGA 689  
 Db 1201 TGGACTCATATATATGTTGACACAGAGTCTCGAAAGCTTATGCTCTGAGCTGA 1260  
 QY 690 TGTGTCAGTGTGTTGTTATCTCTACATTTTACTACGCGTGTCTCTCTCTCTCTGGGC 749  
 Db 1261 TGTGTCAGTGTGTTGTTATCTATCTATCTATCTATTAAGTCGAGTCTCTCTCTCTGGGC 1320  
 QY 750 AGAGCTGAGCTGGAATCTTTAGACAGATATGCAAGGGAAGTTAGATTTCAAACTGA 809  
 Db 1321 TGAATATGACAAAGGAATATTTGAACAGCTCTGACGCGTATCTTACTTACCTCAGA 1380  
 QY 810 CCGCTGGCTTACTATCTCAGAGCTGCTAAGATTTGATCTATTAATGCTCGAAGAGGAG 869  
 Db 1381 CCCATGGCCAAATTTTCAAGAGATGCAAAAGACTTGATGAGGAGAAATGCTCTGTCAGA 1440  
 QY 870 CCCAAGAAACGATTTCTGCTCATGAAGCTTGTGTCACCATGGATTTGTCGATGAACA 929  
 Db 1441 TCCGAGAGAGCTTTAAGTCACATGAAGTTTATGCTCATCTTGGGTACAAAGTTGATGG 1500  
 QY 930 AGCAGACACGACCAAGCTCTTATCCAGAGCTCTATCTCTGCTTAAGAGAGTTTCTCA 989  
 Db 1501 TGTGGCTCCGATAAGCTCTGATTTCTGAGTCTGATGAGTGAAGCAATTTTCTGC 1560  
 QY 990 AATGAATTAAGATTAAGAAATGCTATCGGCTAATGCTGAGAGACTTTTCAGAGGAAGA 1049  
 Db 1561 AATGAACAGCTCAAGAAATGGCTTTGAGAGTCAATGCTGAAGCTTATCCGAGAGAGA 1620  
 QY 1050 AATTGAGGCTGAAGGAATTTGTTCAAGATGATAGACACAGACACAGCGGAAAGATTAC 1109  
 Db 1621 AATTGCTGGTCTTAAAGAAATGTTCAAGATGATAGACACAGACATATAGCGGTCAAAATAC 1680  
 QY 1110 TTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCCGATCTGAACTGATGGAATCAGAAAT 1169  
 Db 1681 TTTTGAAGAGCTCAAGAGTGGTAAAGAGATTTGAGCTTATCTGCTTAAATCTGAGAGTCCGAGAT-1740  
 QY 1170 CAAGTCTCTCATGATCGCGCTGATATCGCAACAGTGTGTACATATAGACTACGAGAAAT 1229

Db 1741 CTATGATCTTATGACAGGAGTGCCTGTTGATTAACAGTGGAAACAATTGATTGTTGAATT 1800  
 QY 1230 CCTAGCAGCAACCTTTACACATGAACAAGATGGAGAGAGAGATTTCTGTTGGCTGCATT 1289  
 Db 1801 TATAGCTGCAACATTTACATATGATACAAAATTTGAAGACAAGATCATCTTTTGTGCTTT 1860  
 QY 1290 TTGGACTTTGCAAGACGGAAGCGGTTTATCCATCGATGAGCTTCAGTCAGCTTG 1349  
 Db 1861 CTGTTACTTCGATAAAGATGGAAGTGGCTACATCACTCGGAGTGAAGCTTCAACAAGCTTG 1920  
 QY 1350 CACAGAGTTTGTCTATGATGATACACCTCTGGAGCAGATCATCAAGGAGATTTGATCTTGA 1409  
 Db 1921 TGAGGAATTTGGCATTTGGGATGTCGCCATGGAAGAAATGATCAGAGAGCTGACCAAGA 1980  
 QY 1410 CAATGACGGAAGATTCGATTTCTCGAGTTTACGCAATGATGAGGAAGGAGATGGAGT 1469  
 Db 1981 CAATGACGCGGCAATGCTACTACATGAGTTTGTGCTATGATGATCAAAAGGGAATCCAGT 2040  
 QY 1470 TGGGAGAACGCAACCATGATGAAGAACTTGAACCTTCAACATTTGCTGATGCTTTTGGAGT 1529  
 Db 2041 GCTAGTGTGTCGAAGAAAGGCTTAGAGCATAGTTTCAGCATTTGGATTCAGAGAGCAGT 2100  
 QY 1530 TGATGTGAAAAATCTGATGACTGACTCATCTCTCCACAAATTTCTGTTTCTTTTCTC 1589  
 Db 2101 AAAACATATAGAGAGCTTGAAGAGGAATTTTCTTCTTAGTGTGTTGCTATATTTT 2160  
 QY 1590 TTTAAATTCGTTTATATATTT 1609  
 Db 2161 CTTGTGGAATTTTCTGTT 2180

RESULT 14  
 ATU31834  
 LOCUS  
 DEFINITION Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 5 (CPK5) mRNA, complete cds.  
 ACCESSION U31834  
 VERSION U31834.1 GI:1399272  
 KEYWORDS  
 SOURCE Arabidopsis thaliana.  
 ORGANISM Arabidopsis thaliana.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 1967)  
 AUTHORS Hrabak E.M., Dickmann L.J., Satterlee J.S. and Sussman M.R.  
 TITLE Characterization of eight new members of the calmodulin-like domain protein kinase gene family from Arabidopsis thaliana  
 JOURNAL Plant Mol. Biol. 31 (2), 405-412 (1996)  
 MEDLINE 96343943  
 PUBMED 8756605

REFERENCE 2 (bases 1 to 1967)  
 AUTHORS Hrabak E.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUL-1995) Estelle Hrabak, Horticulture, University of Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA  
 FEATURES  
 source  
 1. .1967  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia"  
 /db\_xref="taxon:3702"  
 /chromosome="4"  
 1. .1967  
 /gene="CPK5"  
 101. .1771  
 /gene="CPK5"  
 /note="calcium-dependent protein kinase"  
 /codon\_start=1  
 /product="calmodulin-domain protein kinase CDPK isoform 5"  
 /protein\_id="AAB03245.1"  
 /db\_xref="GI:1399273"  
 /translation="MGNSCRSPFKDLDEGNKPEDYSKTSITNLSSNSDHSNPAAD"

IIAQFSDNNNNNSKDPALVPIREPIRMRNPDNQAYVYVGLHKTNRIDYLSRK  
 LOGGFTTLCYCTEIASGVYACKSKRKLISKEDVEDVREIQLMHLAGHSIVT  
 IKGAYEDSLVHLVWELCAGGLPDRIIQRGHYSERKAAELTKIIVGWVACHSLGWM  
 HDLKPENLLVWKKDDPSLKAIIDFLSVFRRQOIITDVGVSYYVAPEVPLKRYGP  
 EADVWTGVLKILLSGVPPFAWETQOQIFDANVLKGYIDFSDPMPVLSOSAKLIR  
 MSLSSFAERLTAHEVRHPWICENGVAEDRALDPVLRKQFQSKAMNKLKMKLVIA  
 ELSSEBIIAGLREMFQMDTNSGATTFDELKAGLRKYGSTLKTDEIHLMDRADVDN  
 SGTIDYSEPIAATIHNLKREHLVAAFOVFDKSGFITIDELQACVHEGNADV  
 LEDIIEVQNDGKIDYGEFVEMQKGNAGVGRRTMNSLNSMRDA"

BASE COUNT 581 a 351 c 466 g 569 t

Query Match 39.4%; Score 688.4; DB 8; Length 1967;  
 Best Local Similarity 67.2%; Pred. No. 1.7e-138;  
 Matches 974; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

Qy	73	ACGAGGCAAAACCTAGACGCTCTTCAAAACACAGTCTTACCATATCAAAACACAGGATTA	132
Db	320	ATGAGCGTAAACACAGCAATCAAGCTTACTATGTTCTGGTCTAAGACACCAACAT	379
Qy	133	AGAGATCAATTAACCTTCTGGGAAAACAGTACAGGCAAGCCCAATTTGGAAACACCTATCTC	192
Db	380	CGTGATATCTATACCTTAGCCGCAAGCTAGGTCAGAGTCAATTTGGAAACGACTTATCTA	439
Qy	193	TGCACAGAGAAATCAACTCGCTGCTTAATACGCTGCAATTCGATCCGGAAGCAAGCTC	252
Db	440	TGTACAGAGATTGCTCAGGCGTTGACTACGCTTGTAGTCAATATCCAAGAGGAATTG	499
Qy	253	GTGTGTCGCGAGGATTAACGAAGATGTAAGCGTGAGATTCAGATCAATGATCATCTCTCT	312
Db	500	ATCTCTAAAGAAGATGTTGAGGATGTTAGAAGGAGATTCAGATAATGATCATCTTAGCT	559
Qy	313	GAGCATCCAAATGTTGTAGATCAAGAGGACTATGAGATTCGGTGTGTTGTCATATT	372
Db	560	GTCACGGTATGTCGACGATTAAGAGGACTTATGAGGACTCTTTGTATGTTCACTT	619
Qy	373	GTTATGAGGTTTGTGAAGTGTGTGAGCTTTTGTATCGGATTTGTTCTAAAGGTCATTTT	432
Db	620	GTTATGAGGCTTTGTGCTGGAGGTGAATTTGTTGATAGGATTAATCAGAGGACATTA	679
Qy	433	AGTGAAGTGAAGCTGTCAGCTTATTAAGAGGATTTCTGGTGTGTTGAGGCTCTCAT	492
Db	680	AGTGAGAGGAAGCTGTGAGCTGACTAAGATCAATTCGGTGTGTTGAGGCGTGTCTAT	739
Qy	493	TCTCTTGTGTATGATGATAGATCTCAAACTCAGAAATTTCTTTGTTGATAGTCTCTAAA	552
Db	740	TGCTTGTGTGATGATGATAGACTTGAGGCTCAGATTTCTTATTGTTAATAGGAT	799
Qy	553	GATGATGATAGCTTAAGCTACGATTTGGTTGTCTGTCTCTATATAGCCAGGACAA	612
Db	800	GATGATTTCTCTCAGAGCTATTGATTTGGGCTATCTGTCTTTTCAAAACAGGCTCAA	859
Qy	613	TATTTATATGAGTATGTTGGAAGTCCGTAATGTTGACAGAGGCTGCTAAAGAAATGT	672
Db	860	ATATTCACTGATGTTGTTGAGTCCATATTATGTTGCTCTGAGGTTTGTCTCAAGCT	919
Qy	673	TATGAGCTGAAATAGATGTTGAGGATGCTGGTGTATTCCTCTACATTTTACTCAGCGT	732
Db	920	TATGGGCTGAAAGCTGATGTTGAGGACTGCTGGTGTATTTGTTATATTGCTTAAGCGGA	979
Qy	733	GTTCTCTCTCTGAGGAGAGCTGAGTCTGGAATCTTTAGACAGATTTTGAAGGGAAG	792
Db	980	GTTCCACCTTTCTGGGCAAGAAACACAGCAAGGATATTGATGCTGTTGTAAGGATAT	1039
Qy	793	TTAGATTTCAAAATCTGACCGTGGCTACTATCTCAGAGCTGCTAAAGATTTGATCTAT	852
Db	1040	ATCGACTTTGAGTCAGACCGCTGGCTGTGATATCCGACAGTGTCTAAAGACTTGATCCG	1099
Qy	853	AAATGCTGAAAGAGGCCCAAGAAACGATTTCTGCTCATGAGCTGTGTCACCCA	912
Db	1100	AGAATGTTATCTCCAGGCTTCAGAGGCTTTGACCGCTCATGAAGCTTTGCGTCATCA	1159
Qy	913	TGATTTGTGATGAAACAGCAGCAGCAGCAAGGCTCTTGTATCCAGCAGTCTTATCTCGT	972

Db	1160	TGATCTGTGAGATGGTGTTCACACAGATAGACACATAGATCCAGCTGTCTTCTCGT	1219
Qy	973	CTAAAGCAGTTTTCTCAATGAATTAAGATTAAGAAATAGCAATTTACGGGTAAATGCTGAG	1032
Db	1220	CTCAAGCAATTTCTGCAATGAATTAACATAAAGAGATGGCTTTCAAGGTTATAGCTGAG	1279
Qy	1033	AGACTTTCAAGAGAGAAATTTGAGGCTTGAAGGATTTGTTCAAGATGATAGACACAGAC	1092
Db	1280	AGTCTCTCGAAGAGAGATGCTGTTTAAAGAGAAATGTTTCAAGCAATGGATCTGAT	1339
Qy	1093	AACAGCGGAACGATTAATTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGGATCTGAA	1152
Db	1340	AACAGCGGGCGATCACTTTGATGAATCAAGCTGAGGCTGAGAAATATGATCTACC	1399
Qy	1153	CTGATGGAATCAGAAATCAAGTCTCTCTGATGGGCTGATATCGACAAAGTGGTACA	1212
Db	1400	TTGAAAGACACAGAGATCCATGATCTTATGGATGGGCTGATGTAGACAAAGTGGGACA	1459
Qy	1213	ATAGACTAGGAGAAATCTCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGAGAG	1272
Db	1460	ATAGATTAAGTGAGTTCATTTGAGGCGATCCATCTCACAACATAGAGCGGGAAGAG	1519
Qy	1273	ATTCTGTGCTGCTCATTTTGGGACTTTTGCAAGAGCGGATTAATACCATCGAT	1332
Db	1520	CATCTTGTTCAGCGTTTCAATATTTTGAACAAGATGGAAGCGGTTTCAACAATTCAT	1579
Qy	1333	GAGCTTCAGTCAGCTTCGACAGAGTTTGTCTATGTATACACCTCTGACGACATGATC	1392
Db	1580	GAGCTACCAACGCGTGTGTTGAACATGGCATGGCTGATGTTTCTTGAAGACATCATC	1639
Qy	1393	AAGGAGATTGATCTTGACAAATGACGGGAAGATCGATTTCTCGAGATTTTACAGCAATGAT	1452
Db	1640	AAAGAGTTTCATCAAAACAATGATGGAAGATTTGATTTGTTGAGATGATG	1699
Qy	1453	AGGAAGGAGATGGATTTGGGAGACGACCAATGATGATGATGATGATGATGATGATG	1512
Db	1700	CAAAAGGAAATCTGCTGTTGGAAGAGGATGAGAAATAGTCTAAACATTAGCATG	1759
Qy	1513	GCTGATGCTT 1522	
Db	1760	AGAGACGCGT 1769	

RESULT 15  
 AC007887/c  
 LOCUS  
 DEFINITION Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome 1, complete sequence.  
 ACCESSION AC007887  
 VERSION AC007887.9 GI:8778333  
 KEYWORDS HTG.  
 SOURCE Arabidopsis thaliana.  
 ORGANISM Arabidopsis thaliana.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 158096)  
 Ecker, J.R.  
 Direct Submission  
 Submitted (22-JUN-1999) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th Street and  
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
 2 (bases 1 to 158096)  
 Ecker, J.R.  
 Direct Submission  
 Submitted (04-OCT-1999) Arabidopsis thaliana Genome Center,  
 Department of Biology, University of Pennsylvania, 38th Street and  
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA  
 3 (bases 1 to 158096)  
 Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,  
 Johnson-Hopson, C., Khan, S., Kim, C., Altati, H., Bei, B., Chin, C.,  
 Chlou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,  
Liu, S., Mukharasy, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,  
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vayenberg, M.,  
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.  
Direct Submission  
Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,  
Department of Biology, University of Pennsylvania, 38th and  
Hamilton Walk, Philadelphia, PA 19104-6018, USA  
On Jun 28, 2000 this sequence version replaced gi:6007863.  
This submission of BAC F1504 is shorter by 1338 bases. The  
original BAC had a Tn10 transposon insertion  
(gb|J01829.1|Tn10IS13) from E. coli located at the junction of  
bases 18229 and 18230 of this submission.

FEATURES  
source  
1..158036  
/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"  
/chromosome="1"  
/clone="F1504"  
528..659  
/notes="hypothetical protein"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.1"  
/protein\_id="AAF79342.1"  
/db\_xref="GI:8778334"  
/translation="MLKANTPLFMNEVNSQSTRIMKYLKSKRITKEESNRDKCK"  
1377..1484  
/notes="hypothetical protein"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.2"  
/protein\_id="AAF79343.1"  
/db\_xref="GI:8778335"  
/translation="MLRIPQLASPKRCSIASTAATSCODQTNMLIV"  
complement(join(2370..2492,2593..2748,2776..2868))  
/notes="similar to ubiquitin-conjugating enzyme E2D 2  
gi|4507775"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.3"  
/protein\_id="AAF79390.1"  
/db\_xref="GI:8778382"  
/translation="MIQGNPGFYASGIFRLDIPEDYPFKPKNVVYNINTEYD  
LFNSTFKPIYHNSIKSGSICDILDKKWTSLTVEKLINKSHVLLSITVLLADPN  
ENDPLAYPEIGOLFKNRRQFD"  
complement(3065..3151)  
/notes="hypothetical protein"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.4"  
/protein\_id="AAF79389.1"  
/db\_xref="GI:8778381"  
/translation="MSVKAKMRRITETFEFKAMSSKASLYSIG"  
complement(join(4475..4581,4720..5001,5076..5106,  
5210..5266))  
/notes="hypothetical protein"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.5"  
/protein\_id="AAF79388.1"  
/db\_xref="GI:8778380"  
/translation="VTMLTNIPLQTLGHLTQDAENNSVFKYTNLFPPTSVPSTLTT  
WTKPTAPFVKCNFDAGHINLSITGWIIDHGSARHGSSIVDHYTPSEATKA  
LLVAMQGTWKYKMIQFEGDSHYLASSEFNSFOADTRNOPPLANLCKNLS"  
join(6536..6622,6671..6964,6989..7075)  
/notes="similar to phosphoenolpyruvate carboxykinase  
(ATP)-like protein emb|CAB38935.1"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.6"  
/protein\_id="AAF79344.1"  
/db\_xref="GI:8778336"

/translation="MISQNFYIARFLCIALEMFCYTEYLSVLYEQAIERYGSLIT  
SNGLTMSGAKTDRREISVLEMLLRMSFGDVRIFILYFGLLIFVDFDFPKGLSN  
IETDETFMVNVRRAVDYLSNLEKILSHSGGCKMGKGDGVALFEELGATF"  
complement(join(9342..9431,9588..9662,9771..9872,  
10106..10186,10437..10811))  
/notes="putative 50S ribosomal protein L21, chloroplast  
precursor sp|P51412|RK21\_ARATH; similar to ESTs  
gb|I45781.1, and gb|AW004148.1"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.7"  
/protein\_id="AAF79387.1"  
/db\_xref="GI:8778379"  
/translation="MASSATILSLCSTPSAHCVNSRRSSTILCSLSPKSLNLAKEPLT  
GLPSSTASIKRIATVAFKAEVSVEAFETDIEAVVSDVSEVTEAKREELFA  
VINWGGKIVFPGRILYDKANDVDDQIVLNKVLVGLTKHTYIGKPKVNTAVH  
AVVESQGLNDKVVVFKYKPKKRYRNHGRQPNTRIRITGITGYEYFASPENAVAGEV  
NL"  
complement(join(11530..11670,11756..11980,12064..12231,  
12303..12418,12517..12669,12759..12902,13095..13225,  
13537..14132))  
/notes="similar to calcium-dependent protein kinase SK5  
sp|P28583|CDPK\_SOYBN; similar to ESTs gb|AW728580.1,  
gb|A1994248.1, and gb|A1997898.1"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.8"  
/protein\_id="AAF79386.1"  
/db\_xref="GI:8778378"  
/translation="METKPNRRPSNTVLPYOTPLRDHYLLGKLGQGGQGTTLCT  
EKSTSNYACKSIPEKLVCREDEDVWREIQIMHLSHPNVVRIAGTVEDSVFHI  
MVEVCGELFDRI VSKGFSEREAVKILITGLVVEACHSLGVSMRKLKQSGFLIST  
PKDDAKLATDFLGVFKYKGLIFLWILDILOLVFWLFWFVSMRKLKQSGFLIST  
GLICFTIARNKRVKVFQDLQGLYDVVGSFYVAPEKCKYGGPDIWVSAGV  
ILYLLSGVPPWATTEGSIIFQILQGLDKPSDPWPTISEAKDLIYKMLRSPKR  
ISAHELCHPWIVDEQAPDKPLDPAVLSRLKQFSQNNKIKMALRVIAKRLSEERIG  
GLKELPKMTDNTSGITITFEELKAGLRVSGELMESIKSLMDAAD:DNSGTDYGEF  
LAATLHMYKEREENLVAAFSVFDKDSGYITIDELOSACTEPCGLCTPLDDMIKEID  
LNDGKIDSEFTAMRKQDGVGRSRTWMKLNINLADAFGVDGEKSD"  
join(17932..18090,19698..19920,20052..20233)  
/notes="similar to En/spm-like transposon protein  
gb|AAC14510.1"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.9"  
/protein\_id="AAF79345.1"  
/db\_xref="GI:8778337"  
/translation="NFKLSSQKQMLFWYAMLKAKCNKYLPSTLCGLPILSGTKYTER  
VLHDFITKVIIGPNELISIDMFDPMTLTFKVHPKLRSDRRYMPHFKGFIGMDGTH  
VPAKVSQRDQRYWNRKKNKGMNLIKGYFYVDGSGYLCGLGYPGROSRYHPHPQNG  
APPYNYKFNRLHFLSLRSVIERIFGV"  
20230..20508  
/notes="hypothetical protein"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.10"  
/protein\_id="AAF79346.1"  
/db\_xref="GI:8778338"  
/translation="MKRYVEDNASRARYDVIRLALVATMALNFKVKNIPDPDFE  
ANCEQGNHQPSTNEEVEYQDDQIMDSRQYMEGIRDIAIWNHNR"  
complement(join(21563..21662,21848..22122,22212..24551,  
24643..24717,24801..24989,25089..25340,25419..25941,  
26020..26227,26306..26741))  
/notes="unknown protein; similar to EST gb|N37451.1"  
/codon\_start=1  
/evidence=not experimental  
/product="F1504.11"  
/protein\_id="AAF79385.1"  
/db\_xref="GI:8778377"  
/translation="MEQSAAPQPTMPLPSPVSEASRDDLOCIGTWIVPPKPVGF  
LCGSIPLADNSFPASFTSALLPSTSSSSSSSSSSSSSYLAICLKLFTFC  
CSWTAPRYQMLPMETDNLNPLITDFDNLPLAAVKSRITGDSKEAVITNSLK  
KCEALVAGSVYIGDEIDVIAFPVILKQIFKIPISKARVSIQVORVQCTIVLNPGRDV

```

EEGKLIERRHNQPKCTKNVDESLFNFAMHVRMEACDIPPTTHREHTEKRSSSSLP
AGENSHDAPDRDLKPAGSKQKODGFIKCEKKSKKNKAGVPEVRKNSQISEKIKS
SDSKSKRGGSEFLRVLFQPHNFRMLQSDLLLSFNKRYAVSLHJWVSEKYTE
LWLEAWLNDVWASVEIAICHTENGIVQVTELLKDIIFILKGISDGPAPHPAVV
QQNGALVFLQSNCKEDPGAYWLYKSAGEDLEQLFDLSIISKNHSSVHNDSSSPS
LIHSGRSDSMFSLGNLYRVGHRLSLVVNDNRNKCFLTCNCLDCLADPHLVVAYR
AHEQFARLILNSDESDLTFFSNGVQVRKIDTLEBALDPTVIADHENEVTFSDK
FTEHDSVNIPLVVRPKLBNVSLKXELLHSDSPSHUTEGSVANVSDTSLDGT
LCOTTSPSSKLSAINHVSAIKSLRWTRLOQSSEOVDAFHDLDPFSKSCGDPDC
ISVQDIRKLPFSKLDRLKWLVLGSEYLSLGEAYKEKQOLHOALNTVELACSLYQ
SNPQFEETLVFSVSNKSLQSKFHRTQVEDLEAKSGSPDLSVELSSTRFLWAKY
WMLVDEIVYFPHILKQBSLRTGTTNHLKXQSEVVKVORLKKKLTYSQNCASC
LYNCSKSDRASASSSSGSSARTVPHSRKNRKLQSNVASKYSRDEVRNVF
KYVENSKEBEETSETGKAVLEQONESKETPFCAKGGIFKYLKSGDKDSESNLL
AALNCVETRRALQELPNCBEPQSVLRKKGWVGNELRNRLKSKELNKADEAFADAI
VAFKVCQHTNVLINCLNGHRRALAEVMPKTEALELHRAFENYOKALGTAKLEY
SKSLRYMAAKTELAVATABASSVDNLKVEVYTOLENTYLRFCMLLANSJTTAARE
QXNILEHDSDDSKSLDKREVLSDASDAIRKALALYESLGEIRQEBARAFYLQLA
RYHKOCCFLFETERQSPKRPESNVIORAKYQALLADNRWQKSMDFYGENIPSMFL
TILIERALSLSLFWQNLNFMSLLEGRHSIKTYAESLRTEDPKLYTKFNAQ
LQWLNKMLALSPLSEBANKSOTCGRSGDSGKRLRELYKTSLNKSLNCLDLNMAHALIQ
ISCSLNKCDSVKHKRVIPQGGSVNVLGS"
join(27313..27574,27603..27721,27735..28416,28568..28584,
29183..29237,29327..29469,29559..29835,29998..30455,
30581..30652,30731..30820)
/notes="hypothetical protein"
/codon_start=1

Query Match      38.1%; Score 666.2; DB 8; Length 158096;
Best Local Similarity 72.4%; Pred. No. 9.8e-134;
Matches 1150; Conservative 0; Mismatches 13; Indels 426; Gaps 5;

QY 595 TTTGCTGCTCTTATAGCAGACAAATATTATATGACGTAGTTGGAAGTCCGTACTA 644
Db 12925 TTGGTTTGTTCCTTTCAGACAAATATTATATGACGTAGTTGGAAGTCCGTACTA 12966

QY 645 TGTTCACACAGAGTCTAAAGAAATGTTATGACCTGAAATAGATGTGGAGTCTCGG 704
Db 12865 TGTTCACACAGAGTCTAAAGAAATGTTATGACCTGAAATAGATGTGGAGTCTCGG 12806

QY 705 TGTATCTCTACATTTTACTCAGCGGTGTTCTCCCTTCGTG----- 747
Db 12805 TGTATCTCTACATTTTACTCAGCGGTGTTCTCCCTTCGTGGCAGGTTAGTCTACTAA 12746

QY 748 ----- 747
Db 12745 AAAAGTAGAGTCTTTTATTTACAAGTTTCGAGTCTTTGTTTGAATGATGATTCCTTT 12686

QY 748 -----GCAGAGACTGAGTCTGGAATCTTTAGACAGATATTTCGAAGGAAGTTA 795
Db 12685 CTCCTTGGCAITGACAGACTGAGTCTGGAATCTTTAGACAGATATTTCGAAGGAAGTTA 12626

QY 796 GATTTCAAATCTGACCCGTGGCTACTACTCTCAGAAGCTGCTAAGATTTTGTATCTABA 855
Db 12625 GATTTCAAATCTGACCCGTGGCTACTACTCTCAGAAGCTGCTAAGATTTTGTATCTABA 12566

QY 856 ATGCTCGAAAGAGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCCTTGT----- 904
Db 12565 ATGCTCGAAAGAGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCCTTGTGTATGTTCA 12506

QY 905 ----- 904
Db 12505 CTTTGTGTTTCATTTGGAATTAGCAACTGTTGTGAATTTGTTTATGTTAAATAATGAGT 12446

QY 905 -----GTACCCCATGATTTGTCGATGAACAGCAGCAC 937
Db 12445 ATTGAGTTTGTCTGAATGTTATATAGTTCACCATGATTTGTCGATGAACAGCAGCAC 12386

QY 938 CAGACAAGCCTCTTATCCAGCAGTCTTATCTGCTCTAAAGCAGTCTTCTCAATGATA 997
Db 12385 CAGACAAGCCTCTTATCCAGCAGTCTTATCTGCTCTAAAGCAGTCTTCTCAATGATA 12326

QY 998 AGATTAGAAATGCGATTACG----- 1019

```

Search completed: February 13, 2003, 19:10:36  
Job time : 4804 secs

```

Db 12325 AGATTAGAAATGCGATTACGGGTATGAATTCGAGTAATATACATTCGCTTTTCTTTA 12266
QY 1020 -----GGTAATTCCTCAGAGACTTTTCAGAGGA 1046
Db 12265 TGTCCAAATCCGTATCTCTGTAACACAGGTAATTCCTCAGAGACTTTTCAGAGGA 12206
QY 1047 AGAAATTTGAGAGTCTGAAGGAATTTGTTTCAAGATGATAGACACAGCAGCGGAACGAT 1106
Db 12205 AGAAATTTGAGAGTCTGAAGGAATTTGTTTCAAGATGATAGACACAGCAGCGGAACGAT 12146
QY 1107 TACTTTTGAAGAGCTCAAGCGGGTTTCAAGAGAGTCTGAACTGATGGAATCAGA 1166
Db 12145 TACTTTTGAAGAGCTCAAGCGGGTTTCAAGAGAGTCTGAACTGATGGAATCAGA 12086
QY 1167 AATCAAGTCTCTCATGGATGC----- 1187
Db 12085 AATCAAGTCTCTCATGGATGCGGTATGAAGAACCAAAACAACTCTTTCTCTTTCAA 12026
QY 1188 -----GGCTGATATCGACAAC 1203
Db 12025 AAACTTTTGTTCCTGTTTAAACATCTCTGTGTGTTGCTCAGAGGCTGATATCGACAAC 11966
QY 1204 AGTGTACAAATAGACTACGAGAAATTCCTAGCAGCAACCTTTACACATGAACAAGATGAG 1263
Db 11965 AGTGTACAAATAGACTACGAGAAATTCCTAGCAGCAACCTTTACACATGAACAAGATGAG 11906
QY 1264 AGAGAGAGATTTCTGTGCTGCTGCATTTTCGGACITTTGACAAAGAGCGGTTATATC 1323
Db 11905 AGAGAGAGAAATCTGTGTGCTGCATTTTCGTACTTTGACAAAGAGCGGTTATATC 11846
QY 1324 ACCATCGATGAGCTTCAGTCAGCTTGACAGAGTTTGTCTATGTGATACACCTCTGGAC 1383
Db 11845 ACCATCGATGAGCTTCAGTCAGCTTGACAGAGTTTGTCTATGTGATACACCTCTGGAC 11786
QY 1384 GACATGATCAAGAGATTTGATCTTGACAAAT----- 1413
Db 11785 GACATGATCAAGAGATTTGATCTTGACAAATGTAACCACTCTCTCTCTCTCTCTTTGT 11726
QY 1414 -----GACGG 1418
Db 11725 TTACCTCTCTCTCAATGTTACTTTTACTATACCGAGAGCTTTTGAATATGTAGACGG 11666
QY 1419 GAAGATCGAATTTCTCGAGTTTACAGCAATGATAGGAAAGAGATGAGATTGGGAGAGAG 1478
Db 11665 GAAGATCGAATTTCTCGAGTTTACAGCAATGATAGGAAAGAGATGAGATTGGGAGAGAG 11606
QY 1479 CAGAACCATGATGAAGAGCTTGAACCTTCAACATTCGTGATGCTTTTGGAGTTGATGGTGA 1538
Db 11605 CAGAACCATGATGAAGAGCTTGAACCTTCAACATTCGTGATGCTTTTGGAGTTGATGGTGA 11546
QY 1539 AAAATCTGATGACTGACTCATCTCTTCCACAATTTCTGTTTTTTCTCTTTAATTTTC 1598
Db 11545 AAAATCTGATGACTGACTCATCTCTTCCACAATTTCTGTTTTTTCTCTTTAATTTTC 11486
QY 1599 GTTTATATTTTGAATTTCTAATTTCTTAAGGATACAAAATATATCTCGGCTCTGTTTTTTCG 1658
Db 11485 GTTTATATTTTGAATTTCTAATTTCTTAAGGATACAAAATATATCTCGGCTCTGTTTTTTCG 11426
QY 1659 TTTCTCTTTTATTTTGTACATGAGCAACTTTCTTAATTTTATCTCTCATATGGATAATT 1718
Db 11425 TTTCTCTTTTATTTTGTACATGAGCAACTTTCTTAATTTTATCTCTCATATGGATAATT 11366
QY 1719 TTGCTTCATATAAAAGTTTTTGAATTC 1747
Db 11365 TTTGCTTCATATAAAAGTTTTTGAATTC 11337

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

DM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 17:37:17 ; Search time 383 Seconds  
(without alignments)  
10272.170 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

Sequence: 1 gatccgggtacattcttc.....tataaaagtttttgatctcc 1747

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

1: /SID32/gcgdata/geneseq/geneseqn-embl/NA1980.DAT.\*  
2: /SID32/gcgdata/geneseq/geneseqn-embl/NA1981.DAT.\*  
3: /SID32/gcgdata/geneseq/geneseqn-embl/NA1982.DAT.\*  
4: /SID32/gcgdata/geneseq/geneseqn-embl/NA1983.DAT.\*  
5: /SID32/gcgdata/geneseq/geneseqn-embl/NA1984.DAT.\*  
6: /SID32/gcgdata/geneseq/geneseqn-embl/NA1985.DAT.\*  
7: /SID32/gcgdata/geneseq/geneseqn-embl/NA1986.DAT.\*  
8: /SID32/gcgdata/geneseq/geneseqn-embl/NA1987.DAT.\*  
9: /SID32/gcgdata/geneseq/geneseqn-embl/NA1988.DAT.\*  
10: /SID32/gcgdata/geneseq/geneseqn-embl/NA1989.DAT.\*  
11: /SID32/gcgdata/geneseq/geneseqn-embl/NA1990.DAT.\*  
12: /SID32/gcgdata/geneseq/geneseqn-embl/NA1991.DAT.\*  
13: /SID32/gcgdata/geneseq/geneseqn-embl/NA1992.DAT.\*  
14: /SID32/gcgdata/geneseq/geneseqn-embl/NA1993.DAT.\*  
15: /SID32/gcgdata/geneseq/geneseqn-embl/NA1994.DAT.\*  
16: /SID32/gcgdata/geneseq/geneseqn-embl/NA1995.DAT.\*  
17: /SID32/gcgdata/geneseq/geneseqn-embl/NA1996.DAT.\*  
18: /SID32/gcgdata/geneseq/geneseqn-embl/NA1997.DAT.\*  
19: /SID32/gcgdata/geneseq/geneseqn-embl/NA1998.DAT.\*  
20: /SID32/gcgdata/geneseq/geneseqn-embl/NA1999.DAT.\*  
21: /SID32/gcgdata/geneseq/geneseqn-embl/NA2000.DAT.\*  
22: /SID32/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT.\*  
23: /SID32/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT.\*  
24: /SID32/gcgdata/geneseq/geneseqn-embl/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1747	100.0	1747	24	Arabidopsis CDPK2
2	1202.4	68.8	1657	24	Arabidopsis CDPK2
3	1183.2	67.7	1506	21	Arabidopsis thalia
4	756.4	43.3	1768	22	Soybean calcium de
5	688.4	39.4	1671	21	Arabidopsis thalia
6	652.6	37.4	2550	22	Cucurbita pepo cal
7	629.8	36.1	2022	22	Vigna radiata.calc
8	597.4	34.2	3054	21	Arabidopsis thalia
9	571.4	32.7	2334	22	Rice calcium depen

10	537.2	30.7	1910	22	AAF74275	Sweet potato calci
11	531.8	30.4	2230	24	ABA91081	Physcomitrella pat
12	523	29.9	1647	22	AAF74281	Liverwort calcium
13	522.8	29.9	1791	22	AAF74284	Carrot calcium dep
14	521.6	29.9	2363	22	AAF74284	Common ice plant c
15	520.2	29.5	2436	22	AAF74273	Soybean calcium de
16	515.6	29.5	2306	22	AAF74272	Maize calcium depe
17	513.4	29.4	1647	22	AAF74282	Liverwort calcium
18	512.6	29.3	2466	15	AAQ66397	Protein kinase cDN
19	509.4	29.2	1836	21	AAQ66397	Arabidopsis thalia
20	507.6	29.1	1723	22	AAF74271	Maize calcium depe
21	501	28.7	2040	22	AAF74278	Rice calcium depen
22	499.2	28.6	1392	21	AAQ66397	Arabidopsis thalia
23	496.8	28.4	2251	22	AAF74276	Tobacco calcium de
24	485.2	27.8	1761	21	AAQ66397	Arabidopsis thalia
25	481.2	27.5	2162	22	AAF74262	Arabidopsis calciu
26	478.2	27.4	1967	22	AAF74280	Strawberry calcium
27	448.2	25.7	455	24	ABL93806	Arabidopsis thalia
28	444.6	25.4	1726	22	AAF74263	Arabidopsis calciu
29	444.4	25.4	2087	22	AAF74266	Arabidopsis calciu
30	405.8	23.2	1133	22	AAQ66397	Tobacco homolog of
31	379.8	21.7	921	20	AAQ66397	Tobacco CDPK cDNA.
32	346.2	19.8	1020	19	AAQ66397	Nucleotide sequenc
33	346.2	19.8	1020	22	AAQ66397	ATCDPK1A PK domain
34	337.6	19.3	1412	21	AAQ66397	Zea mays DNA fragm
35	326	18.7	956	22	AAF74269	Peanut calcium dep
36	299	17.1	1781	21	AAQ66397	Arabidopsis thalia
37	290.6	16.6	798	24	ABK71570	Human dithio polynu
38	277.8	15.9	1387	24	ABA91068	Physcomitrella pat
39	257.2	14.7	2210	22	AAF74279	Potato calcium dep
40	227.4	13.0	955	24	ABN98558	Arabidopsis thalia
41	221.6	12.7	2254	24	ABA91080	Physcomitrella pat
42	220.6	12.6	1785	21	AAQ66397	Arabidopsis thalia
43	204.6	11.7	2202	21	AAQ66397	Arabidopsis thalia
44	189.6	10.9	2374	22	AAH46398	Rice CDPK cDNA (cl
45	183.2	10.5	13114	21	AAQ66397	Rice Gene for resi

ALIGNMENTS

RESULT 1  
ABAO6021  
ID ABAO6021 standard; CDNA; 1747 BP.  
XX  
AC ABAO6021;  
DT  
DT 08-MAR-2002 (first entry)  
DE Arabidopsis CDPK2 encoding polynucleotide SEQ ID NO 2.  
XX Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;  
KW disease resistance; agricultural; pathogen; crop yield; ornamental;  
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;  
KW transgenic; plant; enzyme; gene; ss.  
XX Arabidopsis thaliana.  
OS  
FH Key Location/Qualifiers  
CDS 67..1554  
FT /\*tag= a  
FT /product= "CDPK2"  
XX WO200184911-A1.  
PN  
XX 15-NOV-2001.  
PD  
XX 04-MAY-2001; 2001WO-US14368.  
PF  
XX 05-MAY-2000; 2000US-201925P.  
PR  
XX (GEO ) GEN HOSPITAL CORP.  
PA  
XX

PI Sheen J;  
XX WPI; 2002-062179/08.  
DR P-PSDB; AAM48000.  
DR  
XX  
PT Producing plant having increased disease resistance, comprises  
PT regenerating plant from a non-naturally occurring plant cell  
PT over-expressing a polynucleotide encoding a calcium dependent protein  
PT kinase polypeptide  
XX  
XX Disclosure; Fig 1; 44pp; English.  
XX  
XX The invention relates to producing a plant having increased disease  
XX resistance, comprising providing a non-naturally occurring plant cell  
XX over-expressing a polynucleotide encoding a calcium dependent protein  
XX kinase (CDPK) polypeptide and regenerating a plant from the plant  
XX cell, where the CDPK polypeptide is expressed in the plant, increasing  
XX the resistance of the plant to disease as compared to a  
XX naturally-occurring plant. The method is useful for a variety of  
XX agricultural and commercial purposes including improving a plant's  
XX resistance against plant pathogens, increasing crop yields, improving  
XX crop and ornamental quality and reducing agricultural production costs.  
XX The method facilitates an effective and economical method for in-plant  
XX protection against plant pathogen, reducing or minimising the need for  
XX traditional chemical practices (e.g. application of fungicides,  
XX bactericides, nematocides, insecticides, or viricides) that are typically  
XX used by farmers for controlling the spread of plant pathogens and  
XX providing protection against disease causing pathogens. The method  
XX contributes to the production of high quality and high yield agricultural  
XX products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
XX having reduced spots, blemishes and blotches that are caused by  
XX pathogens, agricultural products with increased shelf-life and reduced  
XX handling costs and high quality and yield crops for agricultural  
XX (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
XX (e.g. fiber crops) purposes. The present sequence is that of Abraxidopsis  
XX thaliana CDPK2 of the invention.  
XX  
XX Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;  
Query Match 100.0%; Score 1747; DB 24; Length 1747;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 AAAGTCATTTTAGTGAGCGTGAGCTCAAGCTTATTAAGACGATTCCTTGGTGTGTT 480  
Qy 481 GAGGCTTGTCATTCCTTGGTGTATGATAGAGATCAAAACCTGAGAAATTCCTGTTT 540  
Db 481 GAGGCTTGTCATTCCTTGGTGTATGATAGAGATCAAAACCTGAGAAATTCCTGTTT 540  
Qy 541 GATAGTCCTAAAGATGATGCTAAAGCTTAAGGCTACCGATTTGGTGTCTGCTCTAT 600  
Db 541 GATAGTCCTAAAGATGATGCTAAAGCTTAAGGCTACCGATTTGGTGTCTGCTCTAT 600  
Qy 601 AAGCCAGGACATATTTATGATGCTAGTGTGAGTGTGCTACTATGTTGCCACGAGGTG 660  
Db 601 AAGCCAGGACATATTTATGATGCTAGTGTGAGTGTGCTACTATGTTGCCACGAGGTG 660  
Qy 661 CTAAGAATAATGTTTANGACCTCAAAATAGATGCTGAGTGTGCTGTTTATCTCTACAT 720  
Db 661 CTAAGAATAATGTTTANGACCTCAAAATAGATGCTGAGTGTGCTGTTTATCTCTACAT 720  
Qy 721 TTACTCAGCGGTGTTCTCCCTCTCTGGGAGAGCTGAGTGTGGAATCTTTAGACAGATA 780  
Db 721 TTACTCAGCGGTGTTCTCCCTCTCTGGGAGAGCTGAGTGTGGAATCTTTAGACAGATA 780  
Qy 781 TTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCTTACTATCTCAGAAAGCTCTAAA 840  
Db 781 TTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCTTACTATCTCAGAAAGCTCTAAA 840  
Qy 841 GATTTGATCTATAAATGCTCGAAGAGCCCAAGAACGCAATTCCTGCTCATGAAGCC 900  
Db 841 GATTTGATCTATAAATGCTCGAAGAGCCCAAGAACGCAATTCCTGCTCATGAAGCC 900  
Qy 901 TTGTGTCACCCATGATGTTGATGAAACAGCAGCAACCAAGCCCTTTGATCCAGCA 960  
Db 901 TTGTGTCACCCATGATGTTGATGAAACAGCAGCAACCAAGCCCTTTGATCCAGCA 960  
Qy 961 GTCTTATCTGCTTAAGAGAGTTTCTCAATGAATAGATTAAGAAATGCGATTACGG 1020  
Db 961 GTCTTATCTGCTTAAGAGAGTTTCTCAATGAATAGATTAAGAAATGCGATTACGG 1020  
Qy 1021 GTAATTCCTGAGAGACTTTTCAGAGGAAGAAATGGAGGTCTCGAAGGAATTTGTTCAAGATG 1080  
Db 1021 GTAATTCCTGAGAGACTTTTCAGAGGAAGAAATGGAGGTCTCGAAGGAATTTGTTCAAGATG 1080  
Qy 1081 ATAGACACAGACAAACGCGGAAGATTAATTTTGAAGAGCTCAAGCGGGTTTGAAGAGA 1140  
Db 1081 ATAGACACAGACAAACGCGGAAGATTAATTTTGAAGAGCTCAAGCGGGTTTGAAGAGA 1140  
Qy 1141 GTCGGATCTGAATGATGGAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGAC 1200  
Db 1141 GTCGGATCTGAATGATGGAATCAGAAATCAAGTCTCTCATGGATCGGCTGATATCGAC 1200  
Qy 1201 AACAGTGGTACAATAGACTACGGAGAAATTCCTAGAGCAACCTTACATGAACAGATG 1260  
Db 1201 AACAGTGGTACAATAGACTACGGAGAAATTCCTAGAGCAACCTTACATGAACAGATG 1260  
Qy 1261 GAGAGAGGAGATTTCTGGTGGTTCGATTTTCGAGCTTTGACAAAGACGGAAGCGTTAT 1320  
Db 1261 GAGAGAGGAGATTTCTGGTGGTTCGATTTTCGAGCTTTGACAAAGACGGAAGCGTTAT 1320  
Qy 1321 ATCCACATCGATGAGCTTCAGTTCAGAGTTGCAAGAGTTGGTCTATGTGATACACCTCTG 1380  
Db 1321 ATCCACATCGATGAGCTTCAGTTCAGAGTTGCAAGAGTTGGTCTATGTGATACACCTCTG 1380  
Qy 1381 GACGACATGATCAAGGAGATTTGATTTGCAATGACGGGAAGATCGATTTCTCGGAGTTT 1440  
Db 1381 GACGACATGATCAAGGAGATTTGATTTGCAATGACGGGAAGATCGATTTCTCGGAGTTT 1440  
Qy 1441 ACAGCAATGATGAGGAAGGAGATGGAGTTGGGAGAGCAAGAACCATGATGAAGAACTTG 1500  
Db 1441 ACAGCAATGATGAGGAAGGAGATGGAGTTGGGAGAGCAAGAACCATGATGAAGAACTTG 1500  
Qy 1501 AACTTCACATGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGACTGACTCATC 1560  
Db 1501 AACTTCACATGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGACTGACTCATC 1560

QY 1561 ATTCTTCCACAAATTTCTGTTTTTTTCTTTAAATTCGTTTATATTTGAATCTTAAT 1620  
 Db 1561 ATTCTTCCACAAATTTCTGTTTTTTTCTTTAAATTCGTTTATATTTGAATCTTAAT 1620  
 QY 1621 TCTAGGATACAAATATATCTGCGTGTGTTTTTGGCTTCCCTTTATTTTGTACAT 1680  
 Db 1621 TCTAGGATACAAATATATCTGCGTGTGTTTTTGGCTTCCCTTTATTTTGTACAT 1680  
 QY 1681 GAGCACTTTCTAAATTTTATCTTCATATGATGATAATTTTGGCTTCATATAAAGTTTTT 1740  
 Db 1681 GAGCACTTTCTAAATTTTATCTTCATATGATGATAATTTTGGCTTCATATAAAGTTTTT 1740  
 QY 1741 GAATTC 1747  
 Db 1741 GAATTC 1747

RESULT 2  
 ABA06022 standard; cDNA; 1657 BP.  
 ID ABA06022 standard; cDNA; 1657 BP.  
 XX AC ABA06022;  
 XX DT 08-MAR-2002 (first entry)  
 XX DE Arabidopsis CDPK4 encoding polynucleotide SEQ ID NO 4.  
 XX KW Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;  
 XX KW disease resistance; agricultural; pathogen; crop yield; ornamental;  
 XX KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;  
 XX KW transgenic; plant; enzyme; gene; ss.  
 XX OS Arabidopsis thaliana.

Key Location/Qualifiers  
 CDS 1..1506  
 FT 1..1506  
 FT /\*tag= a  
 FT /product= "CDPK4"  
 XX WO200184911-A1.  
 XX PD 15-NOV-2001.  
 XX PF 04-MAY-2001; 2001WO-US14368.  
 XX PR 05-MAY-2000; 2000US-201925P.  
 XX PA (GEHO ) GEN HOSPITAL CORP.  
 XX PI Sheen J;  
 XX WI P-PSDB; AAM48001.  
 XX PT Producing plant having increased disease resistance, comprises  
 PT regenerating plant from a non-naturally occurring plant cell  
 PT over-expressing a polynucleotide encoding a calcium dependent protein  
 PT kinase polypeptide  
 XX PS Disclosure; Fig 2; 44pp; English.

The invention relates to producing a plant having increased disease resistance, comprising providing a non-naturally occurring plant cell over-expressing a polynucleotide encoding a calcium dependent protein kinase (CDPK) polypeptide and regenerating a plant from the plant cell, where the CDPK polypeptide is expressed in the plant, increasing the resistance of the plant to disease as compared to a naturally-occurring plant. The method is useful for a variety of agricultural and commercial purposes including improving a plant's resistance against plant pathogens, increasing crop yields, improving crop and ornamental quality and reducing agricultural production costs. The method facilitates an effective and economical method for in-plant

CC protection against plant pathogen, reducing or minimising the need for  
 CC traditional chemical practices (e.g. application of fungicides, typically  
 CC bactericides, nematocides, insecticides, or viricides) that are typically  
 CC used by farmers for controlling the spread of plant pathogens and  
 CC providing protection against disease causing pathogens. The method  
 CC contributes to the production of high quality and high yield agricultural  
 CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
 CC having reduced spots, blemishes and blotches that are caused by  
 CC pathogens, agricultural products with increased shelf-life and reduced  
 CC handling costs and high quality and yield crops for agricultural  
 CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
 CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis  
 CC thaliana CDPK4 of the invention.

XX Sequence 1657 BP; 500 A; 287 C; 384 G; 486 T; 0 other;  
 SQ Query Match 68.8%; Score 1202.4; DB 24; Length 1657;  
 Best Local Similarity 84.1%; Pred. No. 1.6e-262;  
 Matches 1384; Conservative 0; Mismatches 251; Indels 11; Gaps 2;

QY 75 GAAGCCAAACCTAGACGCTCTTCAAAACACAGATTCTACCATATCAAAACACGATTAAAG 134  
 Db 6 GAACCAAACCTAGAGACCTCAACAGTGTTCTTCCATACGAAACCAAGATTAAAG 65  
 QY 135 AGATCATTACCTTTCTGGAAAAAGAGCTAGGCCAAGGCCAATTTGGAAACACCTATCTCTG 194  
 Db 66 AGATCACTATCTCTCGGCAAAAAGAGCTAGGCCAAGGCCAATTTGGAAACACCTATCTCTG 125  
 QY 195 CACAGAGAAATCAACCTCGCTTAATTAGCCTGCAATTCGATCCGAAAGCGAAAGCTCGT 254  
 Db 126 TACAGAGAAATCATCATCAGCTAATTAGCCTTGGAAATCAATCCAAAAGTAAAGCTTGT 185  
 QY 255 GTGTCGCGAGGATTACGAAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGA 314  
 Db 186 ATGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGA 245  
 QY 315 GCATCCAAATGTTGTAGGATCAAAAGGACATTCAGAGATTCGGTGTGTTGTCATATTGT 374  
 Db 246 GCATCCTAATGTTGTAGAAATCAAGGGTACTTATGAGACTCTCTGTTTGTTCATTTGT 305  
 QY 375 TATGAGGTTTCTGAAAGTGTGAGCTTTTTCATCGGATTTGTTCTAAAGGTCAATTTTAG 434  
 Db 306 TATGAGGTTTCTGAAAGTGTGAGCTTTTTCATCGGATTTGTTCTAAAGGGTGTGTTTAG 365  
 QY 435 TGAGCGTGAAGCTGCAAGCTTATTAAGACGATTTCTGGTGTGTTGAGGCTTGTCTATTC 494  
 Db 366 TGAACGTGAAGCTGCTAAAGTTGANTTAAGACTATTCTTGGTGTGTTGAGGCTTGTCTATTC 425  
 QY 495 TCTTGGTGTATGTCATAGAGATCTCAAAACCTGAGAAATTTCTTGTGATAGTCTCTAAAGA 554  
 Db 426 TCTTGGTGTATGTCATAGAGATCTTAAGCCTGAGAAATTTCTTGTGATAGTCTCTCAAGTA 485  
 QY 555 TGATGCTAAGCTTAAGGCTACCGATTTTGGTTTGTCTGCTCTTATTAAGCCAGGACAATA 614  
 Db 486 TGATGCTAAGCTTAAGGCTACAGACTTTTGGTTTGTCTGCTCTTCTACAGCCAGGCGAGTA 545  
 QY 615 TTATATACGCTAGTTGGAAGTCCGCTACTATGTTCCACAGAGGTTCTAAAGAAATGTTA 674  
 Db 546 TCTGTATGATGATTTGGAAGTCCGCTATTAATGTTCCACCTGAGGTTCTGAAGAAATGTTA 605  
 QY 675 TGGACCTGAAATAGATGTTGAGTGTGCTGTTTATCTCTACATTTTCTACAGCGGTGT 734  
 Db 606 TGGACCAAGAGATAGACGTGTGGAGCGCGGTGTTATCTTGTACATCTTACTAAGTGGGGT 665  
 QY 735 TCTCTCCTTCTGGGAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGCTT 794  
 Db 666 TCTCTCCTTCTGGGAGAGAACCAAGCTGAGGAACTTTTAGGAGATATTGCAAGGGAAGAT 725  
 QY 795 AGATTTCAAATCTGACCCCGTGGCCTACTATCTCAGAAGCTGCTAAAGATTTGATCTATAA 854  
 Db 726 AGATTTCAAATCTGATCCGCTGGCCTACTATCTCAGAAGCTGCTAAAGATTTGATTTACAA 785  
 QY 855 AATGCTCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 914

Fri Feb 14 09:44:25 2003

us-09-848-806-2.rng

Db 786 ATGCTCGATAGAGCCCAAGAAAGATTTCTCACAATGAAGCATTTGTGTACCCCTTG 845  
Qy 915 GATTTGCGATGAACAAAGACAGACAGAGCCCTTTGATCCAGAGCTTTATCTCTCT 974  
Db 846 GATTTGTTGATGAACATGCTGCACACAGAGCCCTTCACCCAGCAGCTTTGTCCGACT 905  
Qy 975 AAAGCAGTTTCTCAATCAATGAATTAAGAAATGCGATTTACGGTAAATTGCTGAGAG 1034  
Db 906 TAAGCAGTTCTCGCAATCAATTAATCAAGAAATGCGTTACGAGTAATCGCGGAGAG 965  
Qy 1035 ACTTTCAGAGGAAGAAATGAGAGTCTGAAGAAATGTTCAAGATGATAGACACAGACAA 1094  
Db 966 ACTCTCGGAGGAAGATTTGGTGGTCTGAAGAAATGTTCAAAATGATAGATACAGACAA 1025  
Qy 1095 CAGCGGAACGATTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCGGATCTGAACT 1154  
Db 1026 CAGTGGNACAACTCACCTTTGAAGAGCTTAAGCAGGCTTAAGAGAGTTGGATCTGAATT 1085  
Qy 1155 GATGGAAATCAGAAATCAAGTCTCTCATGATGGGCTGATATCGACACAGTGGTCAAT 1214  
Db 1086 GATGGAATCAGAAATCAAGTCTCTTATGGATGGCGGATATAGACAAACAGTGGACAAAT 1145  
Qy 1215 AGACTCGGAGAAATCTACGACGACCTTACACATGAACAAGATGGAGAGAGAGAT 1274  
Db 1146 AGACTCGGTGAATTTCTACAGCGACATACATATAACAAGATGGAGAGAGAGAA 1205  
Qy 1275 TCTGGTGGCTGCATTTTGGACCTTTGACAAAGACGGAAGGTTATATCACCATCGATGA 1334  
Db 1206 CTGGTGGTGGCTTTTCATACCTTTGATAAAGATGGTAGCGGTATATCACCATTGACGA 1265  
Qy 1335 GCTTCAGTCACTGCTGCACAGATTTGGTCTATGTGATACACCTCTGGACGACATGACAA 1394  
Db 1266 GCCTTCACAGCCTGCACAGATTTGGTCTCTGTGACATCCCTCTTGATGACATGACAA 1325  
Qy 1395 CGAGATTGATCTGACAAATGCGGAAGATCGATTTCTCGGATTTACAGCAATGATGAG 1454  
Db 1326 AGAGATTGATCTTGATAATGACGGAAGATTTGATTTCTCAGAGTTTACTGCTATGATGAA 1385  
Qy 1455 GAAAGGAGATGGATTTGGGAGACGACCAACCATGATGAAGACTTGAACCTTCAACATTGC 1514  
Db 1386 GAAAGGAGATGGTGTGGGAGACGACCACTAAGAGAACTTGAACCTTCAACATTGATGC 1445  
Qy 1515 TGATGCTTTTGGAGTTGATGGTGAATAATCTGATGATGATGATGATGATGATGATGATG 1574  
Db 1446 TGAACCTTTTGGAGTTGA-GGACACACAGCAGCAGCTGCTAAATCTGATGATCACCAGT 1504  
Qy 1575 TCTGTTTTTTCCTTTAAATTCGTTTATATTTTGAATTTCTAATTTCTAAGGATACAAA 1634  
Db 1505 AATTATAATCATCTATATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1554  
Qy 1635 AATATATCTGCTGTTTTTTTGTCTTTTCTTTTATTTTATTTTGTACATGAGCACTTTCTAA 1694  
Db 1555 AAAAAGTGAATCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTCA 1614  
Qy 1695 ATTTTATCTCATATGATATTTT 1720  
Db 1615 ATTTTGTATAAGCATGGATATTTT 1640

RESULT 3  
AAC44687  
ID AAC44687 standard; DNA; 1506 BP.  
XX  
AC  
XX  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43752.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.  
XX EPI033405-A2.  
XX 06-SEP-2000.  
PF 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126788.  
PR 01-APR-1999; 99US-0127482.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 18-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 18-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.

PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-0147303.			
PR	06-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-0147493.			
PR	09-AUG-1999;	99US-0147935.			
PR	10-AUG-1999;	99US-0148171.			
PR	11-AUG-1999;	99US-0148319.			
PR	12-AUG-1999;	99US-0148341.			
PR	13-AUG-1999;	99US-0148565.			
PR	13-AUG-1999;	99US-0148684.			
PR	16-AUG-1999;	99US-0149368.			
PR	17-AUG-1999;	99US-0149175.			
PR	18-AUG-1999;	99US-0149426.			
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
PR	27-AUG-1999;	99US-0151080.			
PR	30-AUG-1999;	99US-0151303.			
PR	31-AUG-1999;	99US-0151438.			
PR	01-SEP-1999;	99US-0151930.			
PR	07-SEP-1999;	99US-0152363.			
PR	10-SEP-1999;	99US-0153070.			
<hr/>					
PR	13-SEP-1999;	99US-0153758.	PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.	PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.	PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.	PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.	PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.	PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.	PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.	PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.	PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.	PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.	PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.	PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.	PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.	PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.	PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.	PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.	PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.	PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.	PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.	PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.	PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.	PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.	PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0160741.	PR	18-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.	PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.	PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.	PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.	PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.	PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.	PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.	PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.	PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.	PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.	PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.	PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.	PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.	PR	26-OCT-1999;	99US-0161360.
PR	28-OCT-1999;	99US-0161920.	PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.	PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.	PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.	PR	29-OCT-1999;	99US-0162142.
<hr/>					
Query Match 67.7%; Score 1183.2; DB 21; Length 1506;					
Best Local Similarity 88.2%; Pred. No. 3.5e-258; Indels 0; Gaps 0;					
Matches 1287; Conservative 0; Mismatches 173;					
QY	75	GAAGCCAAACCTAGAGCTCCTTCAAAACACAGTTCTACCATATCAAAACACACGATTAAAG	134		
Db	6	GAACCAAACCTAGAGACCTCAACAGTGTTCTTCCATACGAAACACCAAGATTAAAG	65		
QY	135	AGATCACTATCTCTCGGCAAAAAGCTAGCCAGGCAATTTGGACACACCTATCTCTG	194		
Db	66	AGATCACTATCTCTCGGCAAAAAGCTAGCCAGGCAATTTGGACACACCTATCTCTG	125		
QY	195	CACAGAGAAATCAACCTCCGCTAATTACGCTGCAATCGATCCGAAAGCGAAAGCTCGT	254		
Db	126	TACAGAGAAATCAATCAGCTAATTACGCTTGAATCAATCCAAACGTAAGCTTGT	185		
QY	255	GTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTGTA	314		
Db	186	ATGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTGTA	245		
QY	315	GCATCCAAATGTTGTAGATCAAAAGGACATTATGAAGATTCGGTGTTTGTTCATATTGT	374		
Db	246	GCATCTTAATGTTGTTAGAAATCAAGGTTACTTATGAAGACTCTGTTTTTGTTCACATTGT	305		
QY	375	TATGAGGTTTGTGAAGCTGTGAGCTTTTGTGCGATTGCTTCTTAAAGGTCATTTTAA	434		
Db	306	TATGGAAGTTTGTGAAGCTGTGAGCTTTTGTGCGATTGCTTCTTAAAGGTTGTTTAA	365		
QY	435	TCAGCGTGAAGCTGTCAAGCTTATTAAGACGATTCCTTGGTGTCTTTCAGGCTTGTCTATC	494		

Db 366 TGAAGCTGAAGCTGCTAAGTGAATTAAGACATATCTTGGTGTGTGGAGCTTGCTATTC 425  
QY 495 TCTTGTGTTTATGATAGAGATCTCAAAACCTGAGAAATTTCTTGTATGATAGTCTTAAGA 554  
Db 426 TCTTGTGTTTATGATAGAGATCTTAAAGCTGAGAAATTTCTTGTATGATAGTCTCAAGTGA 485  
QY 555 TGAATGATAGCTTAAGCTTACGATCGATTTGGTTGGTCTGCTCTTATTAAGCCAGGACAATA 614  
Db 486 TGAATGATAGCTTAAGCTTACGATCGATTTGGTTGGTCTGCTCTTATTAAGCCAGGACAATA 545  
QY 615 TTTATATGAGCTAGTTGGAAGTCCGTAATCTTATGCTCCACAGAGGTGCTTAAAGAAATGTTA 674  
Db 546 TCTGTATGATAGTTGGAAGTCCGTAATCTTATGCTCCACAGAGGTGCTTAAAGAAATGTTA 605  
QY 675 TGAACCTGAAATAGATGCTGAGAGTCTGCTGCTTATCTCTACATTTTACTCAGCGGTGT 734  
Db 606 TGAACCTGAAATAGATGCTGAGAGTCTGCTGCTTATCTCTACATTTTACTCAGCGGTGT 665  
QY 735 TCTCTCCCTTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTTGCAAGGGAAGTT 794  
Db 666 TCTCTCCCTTCTGGGACAGACTGAGTCTGGAATCTTTAGGACAGATATTTGCAAGGGAAGAT 725  
QY 795 AGATTTCAAAATCTGACCCGTGGCTTACTATCTCAGAGCTGCTTAAAGATTTTCAATATAA 854  
Db 726 AGATTTTAAATCTGATCCGTGGCTTACTATCTCAGAGGCTGCTTAAAGATTTTCAATATAA 785  
QY 855 AATGCTCGAAGGAGCCCAAGAAAGCCATTTCTGCTCATGAAGCCTTGTGTACCCCATG 914  
Db 786 AATGCTCGATAGAGCCCAAGAAAGCTATTTCTGCACATGAAGCATTTGTGTACCCCTTG 845  
QY 915 GATTTGCTGATGACAGAGCAGACACAGAAAGCTTCTGATCCAGAGCTTATCTCGTCT 974  
Db 846 GATTTGCTGATGACAGAGCAGACACAGAAAGCTTCTGATCCAGAGCTTATCTCGTCT 905  
QY 975 AAGCAGCTTTTCTCAAAATGAATGAATTAAGAAATGCGATTAACGGTAAATCTCTGAGAG 1034  
Db 906 TAACAGCTTCTCGAAATGAATGAATTAAGAAATGCGATTAACGGTAAATCTCTGAGAG 965  
QY 1035 ACTTTGAGAGAAATTTGAGGCTGTAAGGAAATTTGTTCAAGATGATAGACACAGACAA 1094  
Db 966 ACTCTCGAGAGAGAGATTTGTTGCTGTAAGGAAATTTGTTCAAAATGATAGATACAGACAA 1025  
QY 1095 CAGCGGACGATTTACTTTGAGAGCTCAAGCGGTTTGAAGAGAGTGGATCTGAACT 1154  
Db 1026 CAGTGGAAACATACCTTTGAGAGCTTAAAGAGCTTAAAGAGAGTTGGATCTGATTT 1085  
QY 1155 GATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGAACAGTGGTACAAAT 1214  
Db 1086 GATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGAACAGTGGTACAAAT 1145  
QY 1215 AGACTACGAGAAATCTCTAGCAGCACTTACATGAACAGATGAGAGAGAGAGAT 1274  
Db 1146 AGACTACGAGAAATCTCTAGCAGCACTTACATGAACAGATGAGAGAGAGAGAA 1205  
QY 1275 TCTGTGCTGCTGATTTTGGGCTTTTCACTTTGATAAGATGTTAGCGGTTATATCACCATTGACGA 1334  
Db 1206 CTGTGTGTTGGTCTTTTCACTTTGATAAGATGTTAGCGGTTATATCACCATTGACGA 1265  
QY 1335 GCTTCAGTACGCTTGCAGAGTTGGTCTATGATATGATACACCTCTGACGACATGATCAA 1394  
Db 1266 GCTTCAACAGCCTGCAAGAGTTGGTCTCTGTGACACTCCCTCTTATGATGATGATCAA 1325  
QY 1395 GGAGATTGATCTTGAATGACGGAAGATCGATTTCTCGAGTTTACAGCAATGATGAG 1454  
Db 1326 AGAGATTGATCTTGAATGACGGAAGATCGATTTCTCAGAGTTTACTGCTATGATGAA 1385  
QY 1455 GAAAGAGATGAGTTGGGAGAGCAGAAACCATGATGAGAGACTTTGAACTTCAACATTCG 1514  
Db 1386 GAAAGAGATGAGTTGGGAGAGCAGAAACCATGATGAGAGACTTTGAACTTCAATATAGC 1445  
QY 1515 TGATGCTTTTGGAGTTGATG 1534

Db 1446 TGAAGCTTTTGGAGTTGAGG 1465  
RESULT 4  
AAF74274  
ID AAF74274 standard; DNA; 1768 BP.  
XX  
AC AAF74274;  
XX 04-MAY-2001 (first entry)  
XX  
DE Soybean calcium dependent protein kinase clone #2.  
XX  
KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
KW paraquat; diquat; crop production; ds.  
XX  
OS Glycine max.  
XX  
PN WO200107592-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 26-JUL-2000; 2000WO-GB02876.  
XX  
PR 27-JUL-1999; 99GB-0017642.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Holt CD, White AJ, Michael AJ, Osborn RW;  
XX  
DR WPI; 2001-168549/17.  
XX  
PT Producing herbicide resistance plants by inhibiting calcium dependent  
PT protein kinase in plants or by providing an intracellular vacuolar  
PT transporter capable of transporting agrochemical into plant vacuole  
XX  
PS Claim 18; Page 37; 50pp; English.  
XX  
CC The present invention describes a method of producing plants which are  
CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
CC plants which are resistant to the agrochemical of interest. This is  
CC useful in the production of crops with herbicide resistance.  
XX  
SQ Sequence 1768 BP; 511 A; 325 C; 464 G; 468 T; 0 other;  
Query Match 43.3%; Score 756.4; DB 22; Length 1768;  
Best Local Similarity 70.6%; Pred. No. 1.6e-161;  
Matches 1009; Conservative 0; Mismatches 421; Indels 0; Gaps 0;  
QY 106 GTTCTACCATATCAAAACACACGATTAAAGATCATACCTTCTCGGAAAAGCTAGGC 165  
Db 195 GTTCTCCCGCAGCGCACGACATCCCTGAGGTGACGAGTTGGCGGGAAGCTCGG 254  
QY 166 CAAGGCCAAATTTGGAACACCTATCTGCACAGAGAAATCAACCTCCGCTAATTTACGCC 225  
Db 255 CAGGGCCAAATTCGGGCCACCTTCGAGTGCACGGCGGTGCGAGTGGGAAATTCGCG 314  
QY 226 TGCAAAATCGATCCCGAAGCAAGCTCGTGTGTCGGAGGATTAACAGATGATGCGGT 285  
Db 315 TGCAAGTCGATTCGGAAGCGGAAGCTGCTGTGCAAGGAGGACTACGAGACGTGTGGCG 374  
QY 286 GAGATTCAGATCATGATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGACT 345  
Db 375 GAGATTCAGATTAATGCACACTTGTGGAACACGCCAAGTGTCCGCATCGAAGGACG 434  
QY 346 TATGAAGATTCCGTTGTTGTTATATGTTATGAGAGTTTGTGAAGTGTGTTGAGCTTTT 405  
Db 435 TACGAGGATTCACCGCGGTGCACCTGGTCAATGGAGTTGTGCGAGGTTGAGAGTTGTT 494  
QY 406 GATCGGATTTTCTAAAGGCTCAATTTAGTGAGCGGTGAAGCTGTCAAGCTTATTAGAGC 465  
Db 495 GACAGGATTCGTGCAAGAGGACACTACAGCAGAGACAGCGCGGAGGTTGATTAAGAGC 554

466 ATTCTTGGTGTGTGAGGCTTGTCATCTCTCTGGTGTATGTCATAGAGATCTCAAACT 525  
 555 ATTGTGAGGTGTGTAGGCGGTGTCACCTGCTAGGGGTGTCATAGGAGACCTTAAGCCT 614  
 526 GAGATTTCTTTGTTGATGAGTCTTAAGAGTATGATCTTAAGGCTACCGATTTTGGT 585  
 615 GAGATTTCTTTGTTGATGAGTCTTAAGAGTATGATCTTAAGGCTACCGATTTTGGC 674  
 586 TTGCTGTCTTCTTATPAAGCCAGGCAATATTATATGACGTAGTGAAGTCCGTACTAT 645  
 675 TTGCTGTCTTCTTATPAAGCCAGGCAATATTATATGACGTAGTGAAGTCCGTACTAT 734  
 646 GTTGACACAGAGTCTTAAGAGTATGATCTTAAGAGTATGATCTTAAGGCTACCGATTTTGGT 705  
 735 GTGCGACACAGAGTCTTAAGAGTATGATCTTAAGAGTATGATCTTAAGGCTACCGATTTTGGT 794  
 706 GTTATCTCTTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGGCGAGAGCTGTCTGGA 765  
 795 GTTATCTCTTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGGCGAGAGCTGTCTGGA 854  
 766 ATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAATCTGACCGGTGGCTTACTATC 825  
 855 ATCTTCCGACAGATTTTACTAGGAAATCTTGTATTTCTGAGCCTTGGCCTTAGCAT 914  
 826 TCAGAGCTGCTTAAGATTTGATCTTATAAATGCTTCGAAAGGAGCCCAAGAAACGCATT 885  
 915 TCAGACAGTGCAGGATCTAATTCGGAATGCTTGTATCAAAATCCAAAAACAGGCTT 974  
 886 TTGCTCATGAAGCCTTGTGTCACCCATGATTTGCGATGATGAACAGAGCAGCAGAGCAAG 945  
 975 ACAGACATGAAGTATCTCGCCACCCATGATTTGTATGATCAAAATTCGACCTGATATAA 1034  
 946 CCTCTTGTATGTCAGAGCTTATCTGCTCTAAGAGAGTCTTCTCAAAATGAATAAGTAAG 1005  
 1035 CCTCTTGTATGTCAGAGCTTATCTGCTCTAAGAGAGTCTTCTCAAAATGAATAAGTAAG 1094  
 1006 AAATGCGATTAAGGATTTGCTGAGAGACTTTGAGAGAGAAATTTGAGGCTTGAAG 1065  
 1095 AAGATGCGATTTGAGGATTTGCTGAGAGACTTTGAGAGAGAAATTTGAGGCTTGAAG 1154  
 1066 GAATTTCTCAAGATGATGACACAGACAGCAGGAGGAGGATTTGAGAGAGCTTGAAG 1125  
 1155 GAGTTATTTCAAGATGATGACACAGACAGCAGGAGGAGGATTTGAGAGAGCTTGAAG 1214  
 1126 GCGGGTTGAAGAGAGTGGATCTGAATCTGAATCTGAATCTGAATCTGAATCTGAATCTGAAT 1185  
 1215 GATGGTTGAAGCGAGTGAATCTGAATCTGAATCTGAATCTGAATCTGAATCTGAATCTGAAT 1274  
 1186 GCGGCTGATATCGACACAGTGTGATCAATAGACTAGGAGATTTCTAGCAGCAGCAGCTTA 1245  
 1275 GCTGCGGATATTGATATAAGTGGGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1334  
 1246 CACATGAACAAAGATGAGAGAGAGAGATTTCTGGTGTGATTTCTGGACTTTTGACAAA 1305  
 1335 CATTTAAATGAGCTGAGAGAGAGAGAAACCTAGTGTGGCTTCTCTCTATTTTGACAAA 1394  
 1306 GAGGGAAGCGGTTATATCACCATCGATGAGTCTGATGAGTGTGACAGAGTTTGGTCTTA 1365  
 1395 GATGGCAGTGGTTACATAACCTTGTATGATACACAAAGCTTTGTAAGGACTTTGGTTTA 1454  
 1366 TGTGATACACTCTGAGCAGCATGATCAAGGAGATTTGATTTGACAAATGACGGGAAGATC 1425  
 1455 GATGATATCATATTGACGACATGATCAGGAAATTTGATCAAGATTAACGATGGCAATA 1514  
 1426 GATTTCTCGAGTTTACAGCAATGATGAGAAAGGAGATGAGATTTGGGAGAGAGCAAC 1485  
 1515 GATTTCTCGAGTTTACAGCAATGATGAGAAAGGAGATGAGATTTGGGAGAGAGCAAC 1574  
 1486 ATGATGAGAGCTTGAATTTCAATTTGATGCTTTTGGAGTTGATCG 1535  
 1575 ATGAGAAAAACATAAATTTAAGAGATGCTTCTTGGATTTAGTACAAATCG 1624

RESULT 5  
 AAC42924  
 ID AAC42924 standard; DNA; 1671 BP.  
 XX  
 AC AAC42924;  
 AC  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37370.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway;  
 KW metabolic pathway; promoter; termination sequence; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0129845.  
 PR 19-APR-1999; 99US-0130077.  
 PR 21-APR-1999; 99US-0130449.  
 PR 23-APR-1999; 99US-0130510.  
 PR 28-APR-1999; 99US-0130891.  
 PR 30-APR-1999; 99US-0131449.  
 PR 30-APR-1999; 99US-0132048.  
 PR 04-MAY-1999; 99US-0132407.  
 PR 05-MAY-1999; 99US-0132484.  
 PR 06-MAY-1999; 99US-0132485.  
 PR 06-MAY-1999; 99US-0132486.  
 PR 07-MAY-1999; 99US-0132487.  
 PR 11-MAY-1999; 99US-0132863.  
 PR 14-MAY-1999; 99US-0134256.  
 PR 14-MAY-1999; 99US-0134218.  
 PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
 PR 14-MAY-1999; 99US-0134370.  
 PR 18-MAY-1999; 99US-0134768.  
 PR 19-MAY-1999; 99US-0134941.  
 PR 20-MAY-1999; 99US-0135124.  
 PR 21-MAY-1999; 99US-0135353.  
 PR 24-MAY-1999; 99US-0135629.  
 PR 25-MAY-1999; 99US-0136021.  
 PR 27-MAY-1999; 99US-0136392.  
 PR 28-MAY-1999; 99US-0136782.  
 PR 01-JUN-1999; 99US-0137232.  
 PR 03-JUN-1999; 99US-0137528.  
 PR 04-JUN-1999; 99US-0137502.  
 PR 07-JUN-1999; 99US-0137724.  
 PR 08-JUN-1999; 99US-0138094.  
 PR 10-JUN-1999; 99US-0138540.  
 PR 14-JUN-1999; 99US-0138847.  
 PR 16-JUN-1999; 99US-0139119.  
 PR 17-JUN-1999; 99US-0139453.  
 PR 18-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.  
 PR 18-JUN-1999; 99US-0139460.  
 PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 21-JUN-1999; 99US-0139818.  
 PR 21-JUN-1999; 99US-0139819.  
 PR 21-JUN-1999; 99US-0140353.  
 PR 21-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140695.  
 PR 28-JUN-1999; 99US-0140823.  
 PR 29-JUN-1999; 99US-0140991.  
 PR 30-JUN-1999; 99US-0141287.  
 PR 01-JUL-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142800.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 19-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144633.  
 PR 20-JUL-1999; 99US-0144681.  
 PR 21-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145090.  
 PR 22-JUL-1999; 99US-0145192.  
 PR 23-JUL-1999; 99US-0145144.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 23-JUL-1999; 99US-0145224.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 27-JUL-1999; 99US-0145919.  
 PR 27-JUL-1999; 99US-0145951.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 02-AUG-1999; 99US-0146389.  
 PR 02-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 05-AUG-1999; 99US-0147260.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 08-AUG-1999; 99US-0147493.  
 PR 09-AUG-1999; 99US-0147935.  
 PR 10-AUG-1999; 99US-0148171.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.  
 PR 13-AUG-1999; 99US-0148684.  
 PR 16-AUG-1999; 99US-0149368.  
 PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.

PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 21-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156459.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 39.4%; Score 688.4; DB 21; Length 1671;  
 Best Local Similarity 67.2%; Pred. No. 3.8e-146;

Matches 974; Conservative 0; Mismatches 476; Indels 0; Gaps 0;

Qy 73 ACAGAGCCAAACCTTAGACGTCCTTCAACACAGTTCATCATCAACACACGATTA 132  
 Db 220 ATGAGGCGTAACCCAGACAACTACTATGTTCTTGGTCATAAGACACCAACATT 279  
 Qy 133 AGAGATCATTTACCTTCTGGAAAAAAGCTAGCCAGGCCAAATTTGGAACAACTATCTC 192  
 Db 280 CGTGATATCTATACCTTAGCCGCGAGCTAGGTCAAGTCAATTTGGAACGACTATCTA 339  
 Qy 193 TGCACAGAGAAATCAACCTTCGCTTAATTAGCCTTCAAAATCGATCCGACGGAAGCTC 252  
 Db 340 TGTACAGAGATTGCTTCAGCGCTTACTACGCTTGTAAAGTCAATATCCAGAGGAGTTG 399

QY 253 GTGTGCGGAGGATTACGAAGATGTATGGCTGAGATTGAGATCATCATCTCTCT 312  
 Db 400 ATCTCTAAAGAGATGTTGAGGATGTTAGAAAGGAGATTGAGATTAATGATCATCTAGCT 459  
 QY 313 GAGCATCCAAATGTTTGGATCAAGGAGCTTATGAAGATTGGTGTGTTGTCATATT 372  
 Db 460 GGTGACGGTAGTATCGTACGATTAAAGGAGCTTATGAGGACTCTTTGTATGTTACATT 519  
 QY 373 GTTATGGAGGTTTGTGAAGGTGCTGAGCTTTTTTGTGCGGATTGTTTCTAAAGGTCATTTT 432  
 Db 520 GTTATGGAGCTTTGCTGAGGTGAATTTGTTGATGAGGATTATTGAGAGGACATTAT 579  
 QY 433 AGTGAGGCTGAAGCTGTCAAGCTTATTAGACGATTCTTGGTGTGTTGAGGCTGTGAT 492  
 Db 580 AGTGAGGAGAAAGCTGTGAGCTGACTAAGATCATGTCGGTGTGTTGAGGCGTGTGAT 639  
 QY 493 TCTCTTGGTCTTATGATAGATGATCTCAAACTGTGAAATTTCTTGTGATAGTCTCTAAA 552  
 Db 640 TCGCTTGGTGTGATGATAGACTTTGAGGCTGAGAAATTTCTTATTGTTAATAAGGAT 699  
 QY 553 GATGATGCTAAGCTTAAGGCTACCGATTGTTGGTGTGTTGCTGCTTCTTAAAGCCAGGAAA 612  
 Db 700 GATGATTTCTCTCAAGGCTATTGATTTTGGGCTATCTGTCTTTTCAAAACGAGTCAA 759  
 QY 613 TATTATATGACGTAGTTGGAAGTCCGTAATGTTGACACGAGGTGCTAAAGAAATGT 672  
 Db 760 ATATTCTAGTGTGTTGGAAGTCCATATTATGTTGCTCTGAGGTTTGTCTCAAAGT 819  
 QY 673 TATGACCTGAAATAGATGTTGGAAGTGTGTTGTTATCTCTTACATTTTACTCAGCGGT 732  
 Db 820 TATGGGCTGAAAGCTGATGTTGGAAGTGTGTTGTTATGTTATATTGTTAAAGCGGA 879  
 QY 733 GTTCTCTCTCTGCGGAGAGATGATGCTGGAATCTTTAGACAGATATTGCAAGGGAG 792  
 Db 880 GTCCCACTTTCTGGGCGAGAAACACAGAAAGGATTTTGTGCTGTGTTGAAGGATAT 939  
 QY 793 TTAGATTTCAAATCTGACCGGTGCTCTACTATCTCAGAAGCTGCTAAAGATTGATCTAT 852  
 Db 940 ATGACCTTTGAGTCAGACCGCTGGCTGTGATATCCGACAGTCTAAAGACTTGTATCGC 999  
 QY 853 AAATGCTGAAGGAGGCCCCAAGAAAGCATTTCTGCTCATGAGCCTTGTGTCACCA 912  
 Db 1000 AGAATGTTATCTTCAAGCCTGACAGACGTTTACCGCTCATGAAGCTTTGGGTATCCA 1059  
 QY 913 TGGATTTGATGAACAGACAGACCAAGACGCTCTTGTATCCAGCAGCTTATCTCTGT 972  
 Db 1060 TGGATCTGTGAGATGTTGTCACAGATAGACACTAGATCCAGCTGTTCTTCTGT 1119  
 QY 973 CTAAGCAGTTTCTCAAATGAATAAGATTAAAGAAATGCGCATTTACGGTAAATGCTGAG 1032  
 Db 1120 CTCAGCAATTTCTGCAATGAATAAATAAGAAAGATGCGCTTTGAAGGTTATAGCTGAG 1179  
 QY 1033 AGATTTTCAAGAGGAGAAATGGAGGTCTCAAGAAATTTGTCAGATGATAGACACAGAC 1092  
 Db 1180 AGTCTCTCGGAGAGAGATAGCTGTTTGAAGAAATGTTTCAAGCAATGATGATCTGAT 1239  
 QY 1093 AACAGCGAAGATTACTTTTGAAGACTCAAGCGGTTTGAAGAGATGCGATCTGAA 1152  
 Db 1240 AACAGCGGCGCAATCACATTGATGAATCAAACTAAAGAGATGCGCTTGAGGTTATAGCTAGC 1299  
 QY 1153 CTGATGGAATCAGAAATCAGATCTCTCATGATGCGGCTGATATCGAACACAGTGTGATA 1212  
 Db 1300 TTGAAGACACAGAGATCCATGATCTTATGATGCGGCTGATGATAGACACAGTGGACA 1359  
 QY 1213 ATAGATACGAGAAATCTTAGCAGCACTTACATGAACAAAGATGGAGAGAGAGG 1272  
 Db 1360 ATGATTTACAGTGAATTCATTGACAGCAGCATCTCTCAACAACTAGAGCGGGAAG 1419  
 QY 1273 ATTCTGGGCTGATTTTGGAGCTTTGACAAAGACGGAAGCGTTATATCATCCTCGAT 1332  
 Db 1420 CATCTTGTGAGCGTTTCAATATTTTGAACAAGATGGAAGCGGTTTCAATACAAATTGAT 1479

QY 1333 GAGCTTCAGTCAGCTTGCACAGAGTTGGTCTATGTATACACCTCTGGACGATGATC 1392  
 Db 1480 GAGCTTACACAAAGCTGTGTTGAACATGGCATGGCTGATGTTTCTTGGAGCATCATC 1539  
 QY 1393 AAGGAGATTGATCTTTGACAAATGACGGGAAGATCGATTCTTCGGAGTTTACAGCAATGATG 1452  
 Db 1540 AAAGAGTTGATCAAAAACAATGATGGAAGATTGATTATGTTGAGTTTGGAGATGATG 1599  
 QY 1453 AGAAAGGAGATGGAGTTGGGAGAAAGCAACCATGATGAAGAATTTGAACCTTCAACATT 1512  
 Db 1600 CAAAAGGGAAATGCTGCTGTTTGGAAAGAGGACGATGAGAAATAGCTTAAACATTAGCATG 1659  
 QY 1513 GCTGATGCTT 1522  
 Db 1660 AGAGAGCGCT 1669

RESULT 6  
 AAF74283  
 ID AAF74283 standard; DNA; 2550 BP.  
 XX  
 AC AAF74283;  
 XX  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE Cucurbita pepo calcium dependent protein kinase clone.  
 XX  
 KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
 KW paraquat; diquat; crop production; ds.  
 XX  
 OS Cucurbita pepo.  
 XX  
 PN W0200107592-A2.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 26-JUL-2000; 2000WO-GB02876.  
 XX  
 PR 27-JUL-1999; 99GB-0017642.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Holt CD, White AJ, Michael AJ, Osborn RW;  
 XX  
 DR WPI; 2001-168549/17.  
 XX  
 PT Producing herbicide resistance plants by inhibiting calcium dependent  
 PT protein kinase in plants or by providing an intracellular vacuolar  
 PT transporter capable of transporting agrochemical into plant vacuole  
 XX  
 PS Claim 18; Page 43; 50pp; English.  
 XX  
 CC The present invention describes a method of producing plants which are  
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
 CC plants which are resistant to the agrochemical of interest. This is  
 CC useful in the production of crops with herbicide resistance.  
 CC  
 SQ Sequence 2550 BP; 710 A; 467 C; 627 G; 746 T; 0 other;

Query Match 37.4%; Score 652.6; DB 22; Length 2550;  
 Best Local Similarity 66.6%; Pred. No. 5.5e-138;  
 Matches 934; Conservative 0; Mismatches 469; Indels 0; Gaps 0;

QY 67 ATGAGNCGAGCAACCCCTAGAGTCTTCAACACAGATTTCTACCATATCAACACCA 126  
 Db 843 ATGAAGAGGTTGGTGTGCTGGCTTCGAGGTGTTGAGTTCGATACAGCAAAACGGGA 902  
 QY 127 CGATTAGAGATCATTTACCTTCTTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAAACAAC 186  
 Db 903 AACTTTAAGAGATTTATAGCTTGGGTAATAAATAGGCCAAGGACAAATTTGGGAACA 962  
 QY 187 TATCTGTCACAGAGAAATCAACCTCCGCTAATTAGCCTCGCAATTCGATCCGAGCGGA 246

Db	2043	GAAGATCATCTTCTAGACGGTTTCATATTTTCGACAAAGATCGAAGCGGTTCA	TACC	2102		
QY	1327	ATCGATGAGCTTCAGTCAGCTTCGCACAGAGTTTCGCTCTATGTGATACACCTCTGACGAC	1386			
Db	2103	CACGACGAGCTTCAACAAGCATGTAAAGAGTTTCGGGATAGAGATCTTCAAAATCGAAGAA	2152			
QY	1387	ATGATCAAGAGAGATTGATCTTGCAATCAGCGGAAGATCGATTCTCGGAGTTTACAGCA	1446			
Db	2163	ATGATGCGCAGTCCGATCAAAACATGACCGAAGCATCGACTATACGAGTTCGTGGCG	2222			
QY	1447	ATGATGAGGAAAGAGATGGAGT	1469			
Db	2223	ATGATGCAAAAAGAAATGTAGT	2245			
RESULT 7						
XX	AAAF4285					
ID	AAAF4285	standard; DNA; 2022 BP.				
XX	AAAF4285;					
XX	AC					
XX	DT					
XX	04-MAY-2001	(first entry)				
DE	XX	Vigna radiata calcium dependent protein kinase clone.				
XX	XX					
KW	XX	Calcium dependent protein kinase; CDPK; herbicide resistance;				
KW	XX	paraquat; diquat; crop production; ds.				
OS	XX	Vigna radiata.				
XX	XX					
PN	XX	WO200107592-A2.				
PD	XX					
PD	XX	01-FEB-2001.				
PF	XX	26-JUL-2000; 2000WO-SB02876.				
XX	XX					
PR	XX	27-JUL-1999; 99GB-0017642.				
XX	XX	(ZENE ) ZENESCA LTD.				
PA	XX					
XX	XX	Holt CD, White AJ, Michael AJ, Osborn RW;				
PI	XX					
XX	XX	WPI; 2001-168549/17.				
DR	XX					
PT	PT	Producing herbicide resistance plants by inhibiting calcium dependent				
PT	PT	protein kinase in plants or by providing an intracellular vacuolar				
PT	PT	transporter capable of transporting agrochemical into plant vacuole				
XX	XX					
PS	XX	Claim 18; Page 44-45; 50pp; English.				
XX	XX					
CC	CC	The present invention describes a method of producing plants which are				
CC	CC	resistant to the herbicides paraquat and diquat, involving inhibiting				
CC	CC	the plants a calcium dependent protein kinase (CDPK) and selecting those				
CC	CC	plants which are resistant to the agrochemical of interest. This is				
CC	CC	useful in the production of crops with herbicide resistance.				
XX	XX					
SQ	XX	Sequence 2022 BP; 587 A; 374 C; 466 G; 595 T; 0 other;				
Query Match						
		36.1%;	Score 529.8;	DB 22; Length 2022;		
		Best Local Similarity	65.3%;	Pred. No. 7.5e-133;		
		Matches 925;	Conservative	0; Mismatches 492; Indels 0; Gaps		
QY	116	ATCAACACACGAGTTAAGAGATTCATTACCTTCGGGAAAAAGCTAGCCCAAGGCCAAT	175			
Db	140	ATAAGACTCCCAACATTCGTGATCTATACACTCTTGGCGCAAAATGGGACAGGACAAT	199			
QY	176	TTGGAGAACACCTATCTCTGCACAGAGAAATCAACTCCGCTAATTACGCTCGCAATCGA	235			
Db	200	TTGGCACCACCTTTATATGACCAGAGATTTCTCTTCATGATGATGCTCGCAATCTA	259			
QY	236	TCCCAAGCGAAAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGCGCTGAGATTCAGA	295			
Db	260	TTCTCAAAGAAGAACTGATTTCGAAGGAGGATGTTGAGGATGTCAGGAGGAAATTCAGA	319			





1107	QY	TACTTTTGAAGAGCTCAAAAGCGGGTTTGAAGAGAGAGTCCGATCTCGAACTGATGGGAATCAGA	1166
2634	DB	CACITTTGAAGAACTGAAGAGCAGGACTAAAAACGAGTTTGTGCCAAATCTCAAAGAGTCCAGA	2693
1167	QY	AATCAAGTCTCTCATGGATGGGGCTGATATCGACAAACAGTGGTACAATAGACTACGAGAGA	1226
2694	DB	GATTCTTGTATCTAAATGCAAGCTGCTGATGTGACAAATAGCGGAACGATAGACTACAAAGA	2753
1227	QY	ATTCTTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGAGAGATTCTTGGTGGCTGC	1286
2754	DB	GTTATAGCGGCCACATTCGATCTAAACAAAATAGAGAGAGAGACCATTGTTCGCGCG	2813
1287	QY	ATTTTCGGACTTTGTGACAAAGACGGAGCGGTTTATATACCAATCGATGAGCTTCAGTCAAG	1346
2814	DB	CTTCTCTTACTTTGACAGGACGAGAGTGGCTTTATCACCCCGGACGAGCTTCAACAAGC	2873
1347	QY	TTGCACAGAGTTTGGTCTATGTGATACACCTCTGAGACACATGATCAAGGAGATTGATCT	1406
2874	DB	TTCCGAAGAGTTTGGTGTGAAAGATGCCCGCATAGAGAATGATGCCGATGTTTGATCA	2933
1407	QY	TGACAATGACGGGAAGATCGATTCTTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGG	1466
2934	DB	AGACAAGGATGACAGNATAGACTCAACGAGTTTGTGGCATGATGACGAAGGAGCAT	2993
1467	QY	AGTTGGGGAAGCAGCAACCATGATGAAGAACTTGAACCTTCAACATTGCT	1515
2994	DB	AATGGGAGACCTGTGAAGATGGGTTTAGAGAAACAGCATATAGCATTTTCT	3042

AAF74277  
ID AAF74277 standard; DNA: 2334 bp.

XX  
DT 04-MAY-2001 (first entry)

XX Calcium dependent protein kinase; CDPK; herbicide resistance;  
KW paraquat; diquat; crop production; ds.  
KW

XX  
DN  
W0200107592-A2

01-FEB-2001 PD

XX DE 26-III-2000

PR 27-JUL-1999; 99GB-0017642.

PA (ZENE) ZENECALTD.

XX  
DB WPT: 2001-168549/17.

PT Producing herbicide resistance plants by inhibiting calcium dependent  
 PT protein kinase in plants or by providing an intracellular vacuolar  
 PT transporter capable of transporting agrochemical into plant vacuole  
 XX Claim 18; Page 39; 50pp; English.

resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Query Match 32.7%; Score 571.4; DB 22; Length 2334

Best Local Similarity 62.2%; Pred. No. 1.3e-119;  
Matches 899; Conservative 0; Mismatches 546; Indels 0; Gaps 0;

Qy 91 CGTCCCTTCAACACAGTTTACCATATCAACACACAGGATTAAGAGATCATTTACCTTCTG 150  
Db 531 CCTACATCTATCAATGTCTTGGCGGAGACACAGCGAGCCTTAAGGAGCATTTATATCAT 590

Qy 151 GGAAGAAAGCTAGCCAAAGCCAAATTTGGAAACACCTATCTCTGCACAGAGAAATCAACC 210  
Db 591 GGTGGAGAGCTTGTCTAGGCCAGCTTTGGGACAACTTACCTCTGTACCGAGATCAATACA 650

Qy 211 TCCGCTAATTAAGCTCGCAATCGATCCGAGCGAAAGCTGTGTGTGCGAGAGATAC 270  
Db 651 GGGTGTGATGTCTTCAAGACCATCCCAAGCGCAAGCTCATCAACCAAGGAGATGA 710

Qy 271 GAAGATGTATGGGTGAGATTCAGATCATCATCATCTCTCTGAGCATCAAAATGTTGT 330  
Db 711 GAAGATGTGCGCGGTGAGATTCAGATCATCATCATCTCTCTGAGCATCAAAATGTTGT 770

Qy 331 AGGATCAAGGAGCTTATGAAGATTCGGTGTGTTTGTTCATATTTGTTATGGAGTTCGTAA 390  
Db 771 GCAATCAGGATGTCTAGAGATGGGCAAGCGGTGCACATTTGTGATGAGCTCTCGCT 830

Qy 391 GGTGTGAGCTTTTGTATCGGATTTGTTCTAAGGTCAATTTAGTGTGAGCTGAGCTGTC 450  
Db 831 GGTGGGAGCTTTTGTACAGGATTCAGGAGAGGGGATTCACAGGAGCGGAAGGCTGCA 890

Qy 451 AAGCTTATTAAGACGATTTCTGGTGTGTTGAGGCTTGTCTATCTCTGTGTGTTATGCA 510  
Db 891 GAGCTTATAAGATTAATTTGTGAGCTTGTGCTATGTGCCATTCGCTCGGGGTGATGCA 950

Qy 511 AGAGATCTCAACCTGAGATTTCTTGTGTTGATAGTCTTAAGATGATGCTAAGCTTAAG 570  
Db 951 CGTGTATCTTAAGCCAGAAATTTCTCTCTTTTGGATAAAGATGATGATCTGCTAATAG 1010

Qy 571 GCTACGATTTTGTGCTCTCTCTATAGCCAGGACAAATTTATATGAGCTAGTT 630  
Db 1011 GCAATAGATTTTGTCTATCCGTGTTCTTCAACAGGTCAAGTTTTCAGTGTGTT 1070

Qy 631 GGAAGTCCCTATATGTTGCAACAGAGTGTGTAAGAAATGTTATGACCTGGAATAGAT 690  
Db 1071 GGGAGTCCATATATGTTGCTCTGAGGTATTTGCAACAGCTTATGGACCAAGATCTGAT 1130

Qy 691 GTGTGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCTGGGCA 750  
Db 1131 GTGTGTGAGTGGAGTATCTTTACGTTTCTGAGTGGAGTCCACCATTTTGGGCA 1190

Qy 751 GAGACTGAGTCTGGAATCTTTAGACAGATTAATGCAAGGAGTATGATTTCAATCTGAC 810  
Db 1191 GAGACACACACAGGAATTTTGTATGATGAGTCTTGAAGGGTCAATTTTCAATCTGAT 1250

Qy 811 CCGTGGCTTACTTCTCAGAGCTGCTAAGATTTGATCTATAAATGCTGMAAGGAGC 870  
Db 1251 CCATGGCCAAAGATATCTGACAGTCAAGAGGATCTTTAAGAAATGCTCTCTCATTCG 1310

Qy 871 CCCAAGAAAGCCATTTCTGCTCATAGGCTTGTGTACCCATGGAATGTGATGAAACA 930  
Db 1311 CCTCTGGAGCTTTGAAGGCCCATGAAGTCTTAAGCATCTTGGATCTGTGAAATGGA 1370

Qy 931 GCAGACACAGACAGCTCTTGTATCAGCAGCTTATCTCTGCTAAGCAGTTTCTCAA 990  
Db 1371 GTTCCCACTGATCAGCTCTGGAATCCAGGTGTTATCTCTGGCTCAACAAATCTCTGCA 1430

Qy 991 ATGAATAAGATTAAGAAATGCGATTTACGGGTAAATGCTGAGAGACTTTCAGAGGAAGA 1050  
Db 1431 ATGAACAGTTAAAGAGTTGGCTCTGAGAGTATAGTGTAGGCTCTTTCAGAGGAGG 1490

Qy 1051 ATTGAGGTCTGAAGGAATTTGTTCAAGATGATAGACACAGACAGCGGAGGACGATTACT 1110  
Db 1491 ATTGCTGGTTTAAGAGAAATGTTCAAGCGAGTGGACACAAAAATAGAGGTGTATATCAT 1550

Qy 1111 TTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGATCTGAACTGATGAAATCAGAAATC 1170

Db 1551 TTGGTGTAGCTTTAGAGAAAGTTTAAAGAGATTTGGCGCTGAATTTAAGGATACAGAGATT 1610  
Qy 1171 AAGTCTCTCATGTGCGGCTGATATCGACAACAGTGTGTACAATAGACTACGGGAATTC 1230  
Db 1611 GGTGATATTAATGGAAGCGGCACACAACGACAATAATGTAAACAATCCATTATGAAGAATTT 1670  
Qy 1231 CTAGAGCAACCTTACACATGAACAAGATGGAGAGAGAGATTCTGTGCTGCTGCAATTT 1290  
Db 1671 ATTGCTGCAACTCTACCTCTTAAACAAGATAGAAACGTGAGGAGCACCTGCTGGCAGCTTTT 1730  
Qy 1291 TCGGACTTTTGAACAAGACGGAAGCGGTTATATCAACCATCGATGAGCTTTCAGTCAAGCTTTC 1350  
Db 1731 ACATATTTTGAACAAGATGGAGTGTGTTATATCAAGTTGACAAGCTTCAACGAGCTTGT 1790  
Qy 1351 ACAGAGTTTGTCTATGTGATACACCTCTGGAGCAGATGATCAAGAGATGATCTTGAC 1410  
Db 1791 GGAGAACATAACATGAGGAGTTTCACTCTTGAAGAGATTAITTTCAAGAGTTGATCAAAAC 1850  
Qy 1411 AATGACGGGAGATTCGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGGAGTT 1470  
Db 1851 AATGACGGCCAAATTTGACTACGCGGAATTTGTAGCATGATCAAGGCGAGCAACGTTGA 1910  
Qy 1471 GGGAGAAAGCAACCATGATGAAGAACTTGAACCTTCAACATTTGCTGTGATGCTTTTGAGATT 1530  
Db 1911 CTAGGCTGGCAACAATGGAAGCAGTTTGAATGTAGCATTAAGAGACGCACTCAAGTA 1970

Qy 1531 GATGG 1535  
Db 1971 CATTTG 1975

RESULT 10  
AAF74275  
TD AAF74275 standard; DNA; 1910 BP.  
XX  
AC AAF74275;  
XX  
DT 04-MAY-2001 (first entry)  
XX  
DE Sweet potato calcium dependent protein kinase clone.  
XX  
KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
paraquat; diquat; crop production; ds.  
OS Ipomoea batatas.  
XX  
PN WO200107592-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 26-JUL-2000; 2000WO-GB02876.  
XX  
PR 27-JUL-1999; 99GB-0017642.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Holt CD, White AJ, Michael AJ, Osborn RW;  
XX  
DR WPI; 2001-168549/17.  
XX  
XX Producing herbicide resistance plants by inhibiting calcium dependent  
protein kinase in plants or by providing an intracellular vacuolar  
transporter capable of transporting agrochemical into plant vacuole  
Claim 18; Page 38; 50pp; English.  
XX  
XX The present invention describes a method of producing plants which are  
resistant to the herbicides paraquat and diquat, involving inhibiting in  
the plants a calcium dependent protein kinase (CDPK) and selecting those  
plants which are resistant to the agrochemical of interest. This is  
useful in the production of crops with herbicide resistance.  
XX  
SQ Sequence 1910 BP; 560 A; 348 C; 481 G; 521 T; 0 other;

Query Match		30.7%	Score 537.2	DB 22	Length 1910		
Best Local Similarity		63.2%	Pred. No. 6.8e-112				
Matches 843		Conservative 0	Mismatches 488	Indels 3	Gaps 1		
Qy	131	TAAGAGATCAATACCTCTCTGGGAAAAAGCTAGGCCAAGCCAAATTTGGAACAACCTATC	190				
Db	308	TTAGGGCACATTAACAGTCTGGGAAAAAGCTAGGCCAAGCCAAATTTGGAACAACCTATC	367				
Qy	191	TCTGCACAGAGAAATCAACCTCCGCTAAATACCCCTGCAAAATCGATCCCGAAGCGAAAGC	250				
Db	368	TGTTGATCTGAGATTAGAACTGGAACAGATATGCTGCAAGTCAATTTCCAGAAAAAGC	427				
Qy	251	TCGTGTCTCGGAGGATTAAGAGATGATAGGCGTGGAGATTCAGATCATGCATCTCTCT	310				
Db	428	TTGTGACTAAGGGGATTAAGAGATGATAGGCGTGGAGATTCAGATCATGCATCTCTGA	487				
Qy	311	CTGAGCATCCAAATGTTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGTTGTTCTATA	370				
Db	488	GTGGGAGCCCTAATATTTGTTGAGTTCAAGGGGCTTATGAGGATGCTAATTTCTGTATC	547				
Qy	371	TTGTTATGGAGGTTTGTGAAGTGGTGGAGCTTTTGTATCGGATGTTTCTAAAGGTCATT	430				
Db	548	TTGTGATGGAGTTGTGTGCTGGTGGAGAGCTTTTCGATCGGATTTATGCTAAGGGGCACT	607				
Qy	431	TTAGTGAGCGTGAAGCTGCAAGCTTATTAAGACGATTTCTTGGTGTGTTGAGGCTTGTCT	490				
Db	608	ATAGCGAAAGGCTGCTGCTCTCTTTTGCAGGCTTATAGTGAATGTTGTTTCTATCTGCC	667				
Qy	491	ATTCTCTTGTGTTTATGCATAGAGATCTCAAACTCGAGATTTCTTTGTTGATAGTCCTTA	550				
Db	668	ATTTATGGGCGTGATGCACCGCATTTGAAGCCCGAGAAATTTCTTTGTTCTGTATATAA	727				
Qy	551	AAGATGATCTAAGCTTAAGCTACCAATTTGGTGTGCTGCTCTCTATATAGCCAGGAC	610				
Db	728	CTGAAATGCTGCCCTGAAGGCTACTGATTTGGCTTATCAGTGTTCATGGAAGAGGAA	787				
Qy	611	AATATTATAGCTAGTGTGGAAGTCCGACTATGTTGACACAGAGGTCCTAAAGAAAT	670				
Db	788	GGTGTATAGGATTTAGTCCGAGTCTTACTATGTTGCTCCGAGGCTTTGGGAGAA	847				
Qy	671	GTTATGACCTGAAATAGATGTGTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCG	730				
Db	848	AGTATGGGAAGGAACGCGATCTTTGGAGTGCAGGTGTATGTTGTATTTTACTCAGTG	907				
Qy	731	GTGTTCTCTCCCTCTGGSCAGAGACTGAGTCTGAACTTTTAGACAGATATTCGAAGGGA	790				
Db	908	GTGTCCTCCCTCTGGGCTGAACTGAGCGGGGATCTTTAATGCTATACTTAAAGGAG	967				
Qy	791	AGTTAGATTTCAAACTCTGACCCCTGGGCTACTATCTCAGAAAGTGTCTAAAGATTTGATCT	850				
Db	968	AACTCGACTTCCAAACGAACCTTTGGCCTTCTATATCGAGCATTTGCCAAGGACCTAGTAC	1027				
Qy	851	ATAAATGCTGAAAGGAGCCCCAGAAACGATTTCTGCTCATGAGCCCTTGTGTCACC	910				
Db	1028	GAGGATGCTAGCCCAAGCCGGAAGAGACGCTTACTGCTGCCCGAGGTTCTTGAGCATC	1087				
Qy	911	CATGATTTGTGATGAACAAGCAGCAGCAGCAAGCCCTCTTGATCCAGCAGTCTTATCTCT	970				
Db	1088	CATGATCGGAGAGATGGAGAGCATCTGACAGACCACCTAGATAGCGCTGTTCTCTCAA	1147				
Qy	971	GTCCTAAGCAGTTTCTCAATGAATAGATTAAGAAATAGGCAATACGGGTAAATGCTG	1030				
Db	1148	GAAATGAAGCAATTCAGAGCAATGAACAACTCAAGAACTTGGCCCTGAAGTTTATGTCAG	1207				
Qy	1031	AGAGACTTTCAAGAGGAAGAAATTTGGAGTCTGAAAGGATTTCTCAAGATGATAGACACAG	1090				
Db	1208	AAAATCTCTCAGAAGAGAAATTCATGACTGAAAGCAATGTTTCAAGATATCGACACTG	1267				
Qy	1091	ACAAAGCGGAAAGGATTTTCTTTTGAAGGCTCAAGCGGGTTTGAAGAGAGTGGATCTG	1150				
Db	1268	ACAAAGTGGTCAATTAATACAGGAAGAACTGAAGAGGGATTTGCCCAACTCGGGGCAA	1327				

Qy	1151	AACTGATGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAACAGTGCTA	1210
Db	1328	ATCTCAGAGGCTGAAGTTAAGCAAGTTCATGGAAGCTGCTGATGTAGATGAAATGCT	1387
Qy	1211	CAATGACTACGAGAAATTCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGAGAGG	1270
Db	1388	CGATGACTACATCGAATTCATCTGCTACATGCCAAGCAGCAGGCTAGAAGAGAG	1447
Qy	1271	AGATTCTGGTGGCTGCAATTTTCGGACTTTTGCAAAAGACGGAGCGGTTATATCACCATCG	1330
Db	1448	AAATCTATACAAAGCATTTTCAGTATTTTGATTAAGATAGCAGTGGATTTATCAGAGAG	1507
Qy	1331	ATCAGCTTCAGTCCAGCTTCACAGAGATTTGGTCTATGTGAT---ACACCTCTGGACGACA	1387
Db	1508	ATGAATAGAGACTGCTATGAAGGACACGGATAGCTGATGCACCACTATAAGGAA	1567
Qy	1388	TGATCAAGGAGATTTGATCTTGACAATGACGGGAAGATCGATTTCTCGAGTTTACAGAA	1447
Db	1568	TAATATCTGAAGTCGATGCAGATCATGATGGAAGAAATCAACTATGAAGAGTTTTCACAA	1627
Qy	1448	TGATGAGGAAAGGA	1461
Db	1628	TGATGAGATCAGGA	1641

RESULT 11  
 ABA91081  
 ID ABA91081 standard; cDNA; 2230 BP.  
 XX ABA91081;  
 AC AC  
 XX XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Physcomitrella patens CPK-2 full-length cDNA, SEQ ID NO:26.  
 XX  
 KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;  
 PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;  
 PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;  
 casein kinase homologue-3; CK-3; mitogen-activated protein kinase;  
 MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;  
 MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;  
 calcium-dependent protein kinase-2; CPK-2; overexpression;  
 environmental stress; salinity; drought; temperature; tolerance;  
 transgenic plant; EST; expressed sequence tag; ss.  
 KW  
 XX  
 OS Physcomitrella patens.  
 XX  
 XX WO2001/7356-A2.  
 EN  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-US11435.  
 XX  
 XX 07-APR-2000; 2000US-196001P.  
 XX  
 XX (BADI ) BASF PLANT SCI GMBH.  
 XX  
 XX Da Costa Silva EO, Bohnert HJ, Van Thiel N, Chen R;  
 PI Sarria-Millan R;  
 XX  
 XX WPI: 2002-049153/06.  
 DR  
 DR P-PSDB; AAM52842.  
 XX  
 XX  
 PT New protein, useful for increasing tolerance to environmental stress,  
 PT comprises a Protein Kinase Stress-Related Protein selected from  
 PT Protein kinases, Casein kinase homologs, MAP kinases or calcium  
 PT dependent protein kinases -  
 XX  
 PS Claim 14; Fig 2M; 154pp; English.  
 XX  
 CC Sequences AAM52830-AAM52842 represent novel protein kinase stress-related  
 CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences  
 CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA



XX  
PI Holt CD, White AJ, Michael AJ, Osborn RW;  
XX WPI; 2001-168549/17.  
XX Producing herbicide resistance plants by inhibiting calcium dependent  
PT protein kinase in plants or by providing an intracellular vacuolar  
PT transporter capable of transporting agrochemical into plant vacuole  
XX  
XX Claim 18; Page 42; 50pp; English.  
XX  
XX The present invention describes a method of producing plants which are  
CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
CC plants which are resistant to the agrochemical of interest. This is  
CC useful in the production of crops with herbicide resistance.  
XX  
SQ Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;

Query Match 29.9%; Score 523; DB 22; Length 1647;  
Best Local Similarity 62.7%; Pred. No. 1.1e-108;  
Matches 830; Conservative 0; Mismatches 490; Indels 3; Gaps 1;

QY 141 TTACCTTCGGGAAAGCTAGCCAGGCAATTTGGAACCAACCTATCTCTGCACAGA 200  
DB 240 TTACACCTCGGACGGGAACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 299  
QY 201 GAATCAACCTCCGCTAATTAGGCTCGAATCGATCCGAAGGGAAGCTCGTGTGCG 260  
DB 300 CAAGGTTACAGTGAGCTTTTAGCCTCCAGTCAATTTGCGAAGGGAAGTTGACCAATAA 359  
QY 261 CGAGGATTACGAAGATGATGGCTGGAGATTGAGATCATGATCATGATCATCTCTCTGAGCATCC 320  
DB 360 GGATCACTAGGAGATGTCGAGGGAGTGCAGATCATGATCATGATCATGATCATGATCATGATCATG 419  
QY 321 AAATGTTGTTAGGATCAAGGACCTTATGAAGATTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 380  
DB 420 GAACTTTCGAAATTTGAAGGGGGCTATGAGGATAAACAACACGATGATCTCTGTCATGGA 479  
QY 381 GGTGTTGCAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 440  
DB 480 GCTTGTGCTGGGGAAGTCTTCGACCGGATTTTCAGGGGGGACCTACAGTGGAG 539  
QY 441 TGAAGCTGTCAGCTTATTAAGACGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 500  
DB 540 GGCTGCTGAGCTCATGTAGAACTATAGTCAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 599  
QY 501 TGTATGATAGATCTCAACCTGAGATTTCTGTTGATAGTCTTAAAGATGATGC 560  
DB 600 AGTTATGCAACGGGATCTGAAGCCGAGATTTCTGCTTCTTCAAGCTGGAGAGGATGC 659  
QY 561 TAAGCTTAAGGCTACCGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 620  
DB 660 ACCCTGGAAGGCGGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 719  
QY 621 TGACGTAGTTGAAGTCGTACTATGTTGCAACGAGAGTGTCAAGAAATGTTATGAGC 680  
DB 720 AGATATCGTTGAAGTGGTCTACTGCTGGCCAGAGGTTTGGCTGCTAACTATGAGGCC 779  
QY 681 TGAATATAGATGTTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 740  
DB 780 AGAGGCTGATGTTGGAGTGGCGAGTCTTCTTACATTTCTTGGCGAGTCCCTCC 839  
QY 741 CTCTCGGCGAGAGCTGAGTCTGGAACTCTTTAGACAGATATGCAAGGGAAGTTAGATTT 800  
DB 840 TTTCTGGGCGAGAAACCGAAACAAGGATTTTGTATGCCGTAAATGCAAGGTCATATTTGATTT 899  
QY 801 CAAATCTGACCGTGGCTTACTATCTCAGAGCTGCTAAAGATTTGATCTATAAAGTCT 860  
DB 900 CACTAGTATCTTGGCTTCAATTTCTCAAGGCGGAAGATCTGTTAAAGAGGATGCT 959  
QY 861 CGAAGAGCCCCAAGAAACGATTTCTGCTCATGAAAGCTTTGTTGATCCCATCGATGTT 920

DB 960 CAAACAGAACCCAAAGGAGCGATTGAGGCCCATGAAGTTTTAGTCAACCCATGATGATG 1019  
QY 921 CGATGAACAGCAGCACCAGACAAGCCTTTGATCCACAGATCTTTATCTGCTCTAAAGCA 980  
DB 1020 TGTGACGGAGAGGACACAGACAACCACTTGACAAACCCGTTGTCTAGATTGAAGCA 1079  
QY 981 GTTTTCTCAATCAATTAAGATTAAGAAATGSCATTACGGGTAATTTGCTGAGAGACTTTC 1040  
DB 1080 ATTACCGGTATGAACAGCTCAAGAACTTCTCTGAAGGTTATCGGACAGAGTCTCTC 1139  
QY 1041 AGAGGAAGAAATTTGAGGTTCTGAAGGAATTTGTTCAAGATGATAGACACAGACAACAGCGG 1100  
DB 1140 TGAAGAAGAGATCATCGGATTGAAGGAGATGTTAAAGAGTATGGACACAGACAACAGTGG 1199  
QY 1101 AACGATTAATTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTGGGATCTGACTGATGGA 1160  
DB 1200 TACAATCACCTTCGAGGAGTTGAAGATGCTCTTCAAAAGCAGGAGTCAAACTCGGAGA 1259  
QY 1161 ATCAGAAATCAAGTCTCTCATGATCGGCTGATATCGAACACAGTGGTACATAGACTA 1220  
DB 1260 GTCAGAGTGGCGAGCTAATGSCAGCTCTGATGTTGGATGCAATGGCACTATTGACTA 1319  
QY 1221 CGGAAATTTCTAGCAGCAACCTTACATGAACAGATGGAAGATGGAAGAGAGGAGATTTCTGGT 1280  
DB 1320 CTTGAGGTTTCATAACGGCAACCATGCACTTGAATGAAGATAGAGAGGAAGATCATCTTTA 1379  
QY 1381 GGCTGCAATTTTCGACATTTTGCACAAAGACGGAAGCGGTTATATCACCATCGATGAGCTTCA 1340  
DB 1380 CGCTGCCCTTTTGCAGCAATTTTGTAGGACAGCAGTGGGTTTCACTCCATCGAAGAGCTTGA 1439  
QY 1341 GTCAAGCTTGACAGAGTTTGGTCTATGTGATAC---ACCTCTGGACGACATGATCAAGGA 1397  
DB 1440 ACAGGCTTTAATTAAGCACGGGATGGGAGATCTGATCTCTGAAAGAAATTTATTAGGGA 1499  
QY 1398 GATTGATCTTGACAAATGACGGGAAGATCGAATTTCTCGAGTTTACAGCAATGATGAGGAA 1457  
DB 1500 GTTTGACACTGATCATGATGAGCAATCAACTACGACGAGTTCGTTGCCATGATGCGTAA 1559  
QY 1458 AGG 1460  
DB 1560 AGG 1562

RESULT 13  
AAF74270  
ID AAF74270 standard; DNA; 1791 BP.  
XX  
XX AAF74270;  
XX  
XX 04-MAY-2001 (first entry)  
XX  
XX Carrot calcium dependent protein kinase clone.  
XX  
XX Calcium dependent protein kinase; CDPK; herbicide resistance;  
XX paraquat; diquat; crop production; ds.  
XX Daucus carota.  
XX OS  
XX WO200107592-A2.  
XX  
XX 01-FEB-2001.  
XX  
XX 26-JUL-2000; 2000WO-GB02876.  
XX  
XX 27-JUL-1999; 99GB-0017642.  
XX  
XX (ZENE) ZENECA LTD.  
XX  
XX Holt CD, White AJ, Michael AJ, Osborn RW;  
XX WPI; 2001-168549/17.  
XX Producing herbicide resistance plants by inhibiting calcium dependent

PT	protein kinase in plants or by providing an intracellular vacuolar	
PT	transporter capable of transporting agrochemical into plant vacuole	
XX		
PS	Claim 18; Page 34-35; 50pp; English.	
XX		
CC	The present invention describes a method of producing plants which are	
CC	resistant to the herbicides paraquat and diquat, involving inhibiting in	
CC	the plants a calcium dependent protein kinase (CDPK) and selecting those	
CC	plants which are resistant to the agrochemical of interest. This is	
CC	useful in the production of crops with herbicide resistance.	
XX		
SQ	Sequence 1791 BP; 554 A; 286 C; 448 G; 503 T; 0 other;	
	Query Match 29.9%; Score 522.8; DB 22; Length 1791;	
	Best Local Similarity 61.8%; Pred. No. 1.2e-108;	
	Matches 869; Conservative 0; Mismatches 527; Indels 9; Gaps 2;	
QY	61 CCAAAATGGAGACGAAAGCCAAACCTAGACGTCCTTCAACACAGTTCACCATATCAA	120
Db	251 CTTTCACTTAAGCCAGGCAAGTTTCATAGACCTGAGTCAAAACACTATTTTAGGCAAGCCA	310
QY	121 ACACCAGGATTAAAGAGATCAATACCTTCTGGGAAAAGAGCTAGGCCAAGGCAATTTGGA	180
Db	311 TTGGAAGATATTAGGGGTAAGTATCTCTTGGGAAGAAATTTGGCAGGGGTCAATTTGGT	370
QY	181 ACAACCTATCTCTGACACAGAGAAATCAACCTCCGCTAATTAACGCTGCAATCGATCCCG	240
Db	371 TGTGTATATCAATGTACTGAGAATTCAGTGTCTCAATATATATGCTTGTAACTATTTTA	430
QY	241 AAGCGAAGCTCGTGTGTCGAGAGATTACGAGATGATGCGTGTGAGATTCAGATCATG	300
Db	431 AAGAGAAAGCTTGTAGTAAGAAATGATAGGAGGATTAAGAGGAGATTCAGATTTTG	490
QY	301 CATCATCTCTGAGCATCCAAATGTGTAGGATCAAGGGAGCTTATGAAGATTCGGTG	360
Db	491 CAGCAATTTGAGTGGCAACCGAATATTGGGAGTTTAAAGGTGTTTTGAGGATAGGCAA	550
QY	361 TTTGTTCAATTTGATGAGTTTGTGAGGTGTGAGCTTTTGTGCGAATTTGTTCT	420
Db	551 TCTGTGCACCTTGTGATGAGCTTTGTGCTGTGGGAGTTGTTTGACAGGATTAAGCT	610
QY	421 AAAGGTCAATTTAGTGAGCGTGAAGCTGCAAGCTTATTAAGACGATTCCTTGGTGTGT	480
Db	611 CRAAGGACATTTACTCGAGAGAGCGGCTGCTACGATTTGTAGCAGATTTGTAATGTGTC	670
QY	481 GAGCTTGTCATCTCTGTGGTGTATGATGATGAGATCTCAACCTGAGAATTTCTGT	540
Db	671 CATGTTGTCAATTTATGGGGGTGATGCTAGGGATCTTAAAGCCTGAAAATTTCTGTGT	730
QY	541 GATAGTCTTAAAGATGATGCTAAGCTTAAAGGCTACCGATTTTGGTGTGTCTCTCAT	600
Db	731 TCGAGTAAGGATTAAGATGCAATGCTGAAGGCGACGTATTCGGGTATCTGTCTTCAT	790
QY	601 AAGCCAGGACAAATTTATATGACGTAGTTGGAAGTCCCTACTATGTTGCCACGAGGTG	660
Db	791 GAAGAGGAAAGGTATATCTGTAATATAGTTGGTAGTGTCTTACTATGTTGCTCCTGAAGTA	850
QY	661 CTAAAGAAATGTTATGACCTGAATAGATGCTGAGTGTGCTGTTATCTCTACAT	720
Db	851 CTACAGCTAGTATGAAGAGGATGATATCTGAGCGCTGGAGTTATTTGTATATA	910
QY	721 TTACTCAGCGGTGTCTCTCTCTTCTGGGACAGACTGAGTCTGGAAATCTTTAGACAGATA	780
Db	911 CTACTTAGCGGGGTACCTCCATTTTGGGACAGAAATGAAAAGGAATATTTTGTGCAATA	970
QY	781 TTGCAAGGAAGTTAGATTTCAATCTGACCCGTGCGCTACTATCTCAGAAGCTGTCAA	840
Db	971 CTGAAGAGGATGATTGACTTTGAAAGTGAACCATGCGCATGCTCAACAGTGCAMAA	1030
QY	841 GATTGTGATCTATAAAATGCTCGAAGAGAGCCCAAGAAAGCGCATTTTCTCTCATGAAGCC	900
Db	1031 GACCTTGTTGAAGAAGTGTGACACAGGATCCAAGGAGAGGAGTTACTTCTGCAACAAGTT	1090

QY	901 TTGTGTCACCCATGGATTGCGATGAACAAGCAGCAGCAGCAAGCCTCTTTGATCCAACA	960
Db	1091 CTTGATCATCCCTGGATGAGAGAGGTGGAAGCATCAGACAAGCCAATAGATAGTGA	1150
QY	961 GTCTTATCTCGTCTAAAGCAGTTTTCTCAATGAATTAAGATTAAAGAAATGCGATTACGG	1020
Db	1151 GTCTCTCTCTAGAAATGAAGCAGTTTCAGAGCAATGAACAAGCTCAACCACTTGCATTAAG	1210
QY	1021 GTAATTCTCAGAGACTTTTCAGAGGAGAAATTTGGAGGTCTCTGAAGGAATTTGTTCAAGATG	1080
Db	1211 GTATCTCTGAAGTCTATCCGAGGAGAAATTTAAGGTCTTAAATCCATGTTTGCAAAC	1270
QY	1081 ATAGACACAGACAACAGCGGAACGATTAATTTTGAAGAGCTCAAGCGGGTTTGAAGAGA	1140
Db	1271 ATGGACACGGACAAAAGTGTATCAATCACTTATAGGAATTTGAAATCAGGTTTGGCACGG	1330
QY	1141 GTCGGATCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATCGCGCTGATATCGAC	1200
Db	1331 CTAGCTCAAGCTATCAGAAAGTGGAGTCCACAAATTTGATGATGCTCTGCTGATGTAGAT	1390
QY	1201 AACAGTGGTACAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACATGAACAGATG	1260
Db	1391 GGAAATGGTACAATTTGACTACCTTGAATTTTACTGCTACTATGATAGGCAAGCTT	1450
QY	1261 GAGAGAGAGGAGATTTCTGGTGTGCTTTTCGAGCTTTTGACAAAGCAGGAGCGGTTAT	1320
Db	1451 GAAAGTTATGAGCATC-----AAGCATTTTCAATTTTTCAGAGGATTAAGCGCTTC	1504
QY	1321 ATCACCATCGATGAGTTCAGTTCAGCTTGCACAGATTTGGTCTATGT---GATACACT	1377
Db	1505 ATTCTAAGATGAATCTGGAATCTGCAATGAAAGAGTATGSAATGGTGTGACGAAGCCACT	1564
QY	1378 CTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAGATTCGATTTCTCGGAG	1437
Db	1565 ATCAAGGACATAATCTCTGAAGTAGATTCAATATGATGATGSAAGGATTAATTAAGATGAG	1624
QY	1438 TTTCAGCAATGATGAGGAAAGGA	1461
Db	1625 TTCTGTGCGATGATGAGAAGGCA	1648
RESULT 14		
AAF74284		
ID	AAF74284 standard; DNA; 2363 BP.	
XX		
AC	AAF74284;	
XX		
DT	04-MAY-2001 (first entry)	
XX		
DE	Common ice plant calcium dependent protein kinase clone.	
XX		
KW	Calcium dependent protein kinase; CDPK; herbicide resistance;	
KW	paraquat; diquat; crop production; ds.	
XX		
OS	Mesembryanthemum crystallinum.	
XX		
PN	WO200107592-A2.	
XX		
PD	01-FEB-2001.	
XX		
PF	26-JUL-2000; 2000WO-GB02876.	
XX		
PR	27-JUL-1999; 99GB-0017642.	
XX		
PA	(ZENE ) ZENECA LTD.	
XX		
PI	Holt CD, White AJ, Michael AJ, Osborn RW;	
XX		
DR	WPI; 2001-168549/17.	
XX		
PT	Producing herbicide resistance plants by inhibiting calcium dependent	
PT	protein kinase in plants or by providing an intracellular vacuolar	
PT	transporter capable of transporting agrochemical into plant vacuole	

XX  
PS  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
XX  
SQ

Claim 18; Page 43-44; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Sequence 2363 BP; 718 A; 435 C; 542 G; 668 T; 0 other;

Query Match 29.9%; Score 521.6; DB 22; Length 2363;  
Best Local Similarity 60.3%; Pred. No. 2.5e-108;  
Matches 898; Conservative 0; Mismatches 584; Indels 6; Gaps 2;

74 CGAAGCCAAACCTAGACGCTCTTCAAAACACAGTCTTACCATATCAAAACACACACGATTA 133  
Db 523 CAAACACAGCCCAAAAGTTGAGCCAAATACAAATTTGGTAAACCCCTTTGAGGATGTA 582  
Qy 134 GAGATCAATTAACCTTGGGAAAMAAOCTAGGCCAAGGCCAAATTTGGAAACACCTATCTCT 193  
Db 583 AGGTGTACTACACATTTGGGAGAGAACTGGGTAGGGGTCAATTTGGGGTTACCTATCTGT 642  
Qy 194 GCACAGAGAATCAACTCGCTCGCTAATTAAGCTGCAATCGATCCGGAAGCAAGCTCG 253  
Db 643 GCATGACAAAAGACTGGCCACATATGCTTGCAGTCAATCTCTAAGAGAGCTTG 702  
Qy 254 TGTGTCGGAGGATTAAGAGATGATAGCGGTGAGATTGAGATCAATGATCAATCTCTCTCTG 313  
Db 703 TGACCAAGGCTGATAGGATGATGAGGAGAGAGATTGAGATCAATGATCAATCTCTCTCTG 762  
Qy 314 AGCATCAAAATGTTTGGATCAAAAGGACTTATCAAGATTCGGTGTGTTGTTCAATTTG 373  
Db 763 GTCAACCTAATTTGGAATTTAAGGGTCTTATGAGGATTAATGCTAAGGGCCATTATA 822  
Qy 374 TTATGAGGTTTGTGAAGGTGAGCTTTTATCGGATGTTTCTTAAAGTCAATTTA 433  
Db 823 TGATGGAGCTTTGCTGTGGGGAGTTGTTGATAGGATTAATGCTAAGGGCCATTATA 882  
Qy 434 GTGAGCTGAAGCTGCAAGCTTATTAAGACGATTCCTGGTGTGTTGAGGCTGTCATTT 493  
Db 883 GTGAAAAGGCTGCTGCCACTATGTTGAGGAGATTTGTTAAGTTGTTTCTATGTTGTTCT 942  
Qy 494 CTCCTGTGTTTATGATAGAGATCTCAAACTCGAGATTTCTTGTGTTGATGCTCTAAAG 553  
Db 943 TTATGGGTGTGATGATAGGATCTGAAGCTCGAGAACTTCTGCTCTAGCAAGGATG 1002  
Qy 554 ATGATGCTAAGCTTAAGCTACCGATTTTGGTGTGTTGCTGCTCTATTAAGCCAGGACAT 613  
Db 1003 AGAATCTCTTGAAGGCCACTGATTTGGGTGTTGTTGTTTATGAAGAGGTAAG 1062  
Qy 614 ATTTATATGAGTGTGGAAGTCCGTACTATGTTGACCCAGAGGTGCTAAAGAAATGTT 673  
Db 1063 TCTACCGGATATAGTAGGAGTGTCTTACTATGCTGCTCTGAGGATTTGCGTGTAGT 1122  
Qy 674 ATGACCTGAAATAGATGTGAGTGTGCTGCTGTTATCTCTACATTTTACTCAGCGGTG 733  
Db 1123 ATGGAGGAGATTTGATTTGGAGTCTGAGTCTGATTTGTTGATCTTACTCAGTGTG 1182  
Qy 734 TTCTCTCTCTCTGGCAGAGACTCAGTCTGGAATCTTTAGACAGATATTGCAAGGAGT 793  
Db 1183 TGCCCCCTTTTGGCAGAACACGAGAAAGGATCTTTGATGCTATTTTGAAGGCCATA 1242  
Qy 794 TAGATTTCAATCTGAACCCGTGGCTCTATCTCAGAGCTGCTTAAAGATTTGATCTATA 853  
Db 1243 TTGATTTGAAAGCAAAACATGGCCATCAATTTCAATTTGTTGTCAGGACCTAGTGAGAA 1302  
Qy 854 AAATGCTGAAAGAGAGCCCAAGAAAGCATTTCTGCTCATGAAGCTTTGTGTCACCCAT 913  
Db 1303 AAATGTTGACAGAGATCCCAAGAAAGCGATTTACTGCTCTCAAGTTCTTGAGCACCCAT 1362  
Qy 914 GGATTTGATGAACAGCAGCACCCAGCAAGCTCTTGTATCCAGAGCTTTATCTGCTG 973

Db 1363 GGCTAAGAGATGGTGAAGCAT---CAGACAAAGCCAAATAGACAGTGTGTTCTCTCTCAGGA 1419  
Qy 974 TAAAGCAGTTTTTCTCAAAATGAATTAAGAAAATGGCATTACGGGTAAATTTGCTCAGGA 1033  
Db 1420 TGAAGCAATTCAGAGTCTATGAACAGCTCAAGAGCTCGCTCAAGAGTCAATTTGCTGAAA 1479  
Qy 1034 GACTTTAGAGGAAGAAATTTGGAGTCTGAGGAAATTTGTTCAAGATGATAGACACAGACA 1093  
Db 1480 ATCTTTCTCTGATGAAGAGATCCAAAGGCTGAAACAAATGTTTCGGCAATATGGACACTGATG 1539  
Qy 1094 ACAGCGGAACGATTAATTTTGAAGAGCTCAAAAGCGGTGTTTGAAGAGAGTGGGATCTGAAC 1153  
Db 1540 GTAGTGGGTCAATTAATTTTGAAGAGCTGAGGAGGATTTGGCTCGACTTGGATCAAAGC 1599  
Qy 1154 TGATGGAATCAAGAAATCAAGTCTCTCATGGATGCGGTGATATCGACAAACAGTGTACAA 1213  
Db 1600 TTACTGAACTGAAGTGAAGCGCTCATGGAAGCTGCTGATCAAGATGGAAGTGGATCAA 1659  
Qy 1214 TAGACTAGCGGAATTTCTAGCAGCAACCTTACACATGAAACAGATGAGAGAGAGAGA 1273  
Db 1660 TAGACTATGATGATTTTACAGCCACAAATGCAATAGGTACAGTTAGAGAGATGAGC 1719  
Qy 1274 TTCTGTGGCTGCATTTTGGACTTTTGAAGAGCGGATTTATCCATCGATG 1333  
Db 1720 ATCTTTTACAAGGCATTTCCAATATTTTGAAGAGCAATAGTGGTGTATTCACAAACAGATG 1779  
Qy 1334 AGCTTCAGTCAGCTTGCAGAGATTTGCTGATGAT---ACACCTCTGGACGACATGA 1390  
Db 1780 AACTAGAACACCAATGAAGATGATGGATTTGCTGATGAGAAATGCAATTCAGAGATAT 1839  
Qy 1391 TCAAGAGATTTGATTTTGAATGACGGGAAGATGATTTCTCGAGTTTACAGCAATGA 1450  
Db 1840 TGTGGAAGTGAAGTCTGATATGATGGAAGAAATAAATGATGATGAGTTCAAGCGCAATGA 1899  
Qy 1451 TGGGAAAGAGATGAGTCTGGGAGAGCAGAACCATGATGAAGACCTGAACCTCAACA 1510  
Db 1900 TGGAAGTGGGACTCAAAACCCGGTTCACAACTCATTTAGTGTGATGTCGATTTCTAGCA 1959  
Qy 1511 TTCTGATGCTTTTGGAGTTGATGTTGAAATCTGATGACTGACTCA 1558  
Db 1960 CTGTATACGTAAACGCTTTTAAAGTACCAAGGTTTGAACAGTCA 2007

RESULT 15  
AAF74273  
ID AAF74273 standard; DNA; 2436 BP.  
XX  
AC AAF74273;  
XX  
DT 04-MAY-2001 (first entry)  
XX  
DE Soybean calcium dependent protein kinase clone #1.  
XX  
KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
KW paraquat; diquat; crop production; ds.  
XX  
OS Glycine max.  
XX  
FN WO200107592-A2.  
XX  
PD 01-FEB-2001.  
XX  
PF 26-JUL-2000; 2000WO-GB02876.  
XX  
PR 27-JUL-1999; 99GB-0017642.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Holt CD, White AJ, Michael AJ, Osborn RW;  
XX  
DR WPI; 2001-168549/17.  
XX  
PT Producing herbicide resistance plants by inhibiting calcium dependent

PT protein kinase in plants or by providing an intracellular vacuolar  
PT transporter capable of transporting agrochemical into plant vacuole -  
XX  
PS Claim 18; Page 36-37; 50pp; English.

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 17:50:37 ; Search time 75 Seconds  
(without alignments)  
7143.524 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

Sequence: 1 gatccgggtacatatcttc.....tataaaagttttgaattcc 1747

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	429.8	24.6	1349	1	US-07-951-715A-20
2	429.8	24.6	1349	2	US-08-459-448A-20
3	429.8	24.6	1349	3	US-08-459-595A-20
4	429.8	24.6	1349	4	US-08-459-504B-20
5	429.8	24.6	1349	5	US-09-547-442-20
6	429.8	24.6	1349	6	US-08-459-444-20
7	218	12.5	4162	2	US-08-459-448A-26
8	218	12.5	4162	3	US-08-459-595A-26
9	218	12.5	4162	3	US-08-459-504B-26
10	218	12.5	4162	3	US-08-459-444-26
11	218	12.5	4162	4	US-09-547-422-26
12	218	12.5	4165	1	US-07-951-715A-26
13	189.6	10.9	2374	4	US-09-347-801-3
14	165	9.4	1400	1	US-08-464-164-1
15	165	9.4	1400	1	US-08-338-057-1
16	165	9.4	1400	2	US-08-668-416-1
17	129.8	7.4	1776	3	US-08-655-352-10
18	129.8	7.4	1776	4	US-09-258-016-10
19	129.8	7.4	1776	4	US-09-257-825B-10
20	117	6.7	2061	4	US-09-800-960-1
21	114	6.5	2514	3	US-08-655-352-1
22	114	6.5	2514	4	US-09-258-016-1
23	114	6.5	2514	4	US-09-257-825B-1
24	104.2	6.0	1282	2	US-08-876-989-12
25	104.2	6.0	1282	4	US-08-272-796-12
26	98.2	5.6	3471	2	US-08-715-568A-2
27	92.6	5.3	498	4	US-09-347-801-7

Sequence 2, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 9, Appli  
Sequence 37, Appli  
Sequence 36, Appli  
Sequence 3, Appli  
Sequence 44, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-07-951-715A-20

; Sequence 20, Application US/07951715A

; Patent No. 5625136

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/951,715A

; FILING DATE: 25-SEP-1992

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8615

; TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1226  
OTHER INFORMATION: /note= "cDNA sequence for maize  
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as  
OTHER INFORMATION: disclosed in Figure 30."  
US-07-951-715A-20

Query Match 24.6%; Score 429.8; DB 1; Length 1349;  
Best Local Similarity 60.3%; Pred. No. 1.4e-99;  
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 290 TTCAGATCATGATCTCTCTGAGCATCCAAATGTTGTAGGATCAAGGACATTATG 349  
Db 1 TGCAGATCATGACACCTCTCCGGCAGCCCAACGTTGGTGGCCCTCGCGGCGGTACG 60  
QY 350 AAGATTCGGTGTGTTTCATATGTTATGAGAGTTTGTGAAGTGTGTGAGCTTTTGTATC 409  
Db 61 AGGACAAGCAGAGCGTGACCTCTCATGAGCTGTGCGCGGGGGAGCTCTTCGACC 120  
QY 410 GGATTTGTTTAAAGGTCTATTTAGTAGCGTGAAGTGTCAAGCTTATTAAAGACCATTC 459  
Db 121 GCAATCATGCCCGGGCCAGTACACGAGCGCGCGCGGAGCTCTCGCGGCCATCG 180  
QY 470 TTGGTGTGTTGAGGCTGTGATTCCTTGTGTTGTTATGATAGATCTCAAACCTGAGA 529  
Db 181 TGCAGATCTGACACCTGCCACTCCATGGGGTGATGACACCGGGAGCATCAAGCCCGAGA 240  
QY 530 ATTCTTGTGTTGATGCTCTAAAGATGATGTTAAGCTTAAGCTACCGATTTTGTGTTGT 589  
Db 241 ACTTCTGTGCTGACGAAGGACGAGGACGCGCCCTCAAGCCACCGACTTCGGCTCT 300  
QY 590 CTGCTCTTATAAGCCAGGACATATTTATATGAGTGTGTTGGAAGTCCGTTACTATGTTG 649  
Db 301 CGTCTCTTCAAGGAGGCGAGTCTCAGGACATCGTCCGAGCGCCCTACTACATCG 360  
QY 650 CACGAGGTCTAAAGAAATGTTATGAGCTGTAATAGTGTGTTGAGTCTGCTGTGTTA 709  
Db 361 CGCCCGAGTCTCAAGAGGAAGTACGGCCCGGAGCGCGCATCTGGAGCGTGGGTCA 420  
QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGGCGAGACTGAGTCTGGAATCT 769  
Db 421 TGCTCTACATCTCTCTCGCGGGTGCCTCCCTTCTGGGCGAGAACGAGAACGGCATCT 480  
QY 770 TTAGACAGATATTGCAAGGAGTTAGATTTCAATCTGACCGGTGGCTACTATCTCAG 829  
Db 481 TCACCGCCATCTCGGAGGGGAGCTGAGCTCTCAGCGAGCATGGCCACATCTCGC 540  
QY 830 AAGCTGCTAAGATTTGATCTATAAATGCTCGAAGAGGAGCCCAAGAAAGCCATTTCTG 889  
Db 541 CGGAGCCAGAGTCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGGCTCAAGG 600  
QY 890 CTCAATGAGCTTGTGTCACCCATGATTGTGATGAACAGCAGCACCAGACAGGCTTC 949  
Db 601 CGTTCAGGTCCTCAATCAACCCATGATCAAAAGAGCAGGAGCGGCTGACAGCGCGC 660  
QY 950 TTGATCCAGAGCTTATCTGCTCTAAGCAGTTTCTCAATGAATGAATTAAGAAAA 1009  
Db 661 TTGACACAGTGTCTCGACAGGCTCAAGAGTTCAGGCGCATGACCAAGTTCAGAAAG 720  
QY 1010 TGGCATTACCGGTAATTTGTGAGAGACTTTTCAGAGGAAGAAATTTGAGGTCTGAAGGAT 1069  
Db 721 CAGCATTGAGGATCATAGCTGGTGGCTATCCGAAGAGGAGATCAAGGGCTGAAGGAA 780  
QY 1070 TGTTCAAGATGATAGACAGACACAGCGGAACGATTACTTTGAAGAGCTCAAGGCGG 1129

Db 781 TGTTCAAGAACATTGCAAGGATAACAGGGGACCATTTACCTCGACGAGCTCAACACG 840  
QY 1130 GTTTGAAGAGAGTCGGATCTGAATGATGGAATCAGAATCAAGTCTCTCATGGATCGG 1189  
Db 841 GGTTCGAAGACACGGGCCAAGCTGTGACAGCAGGAATGGAGAACTAATGGAAGCAG 900  
QY 1190 CTGATATCGACAACAGTGTGATCAATAGACTACGAGAAATTTCTAGCAGCAACCTTACACA 1249  
Db 901 CTGACGCTGACGCAACAGGCTTAAATTGACTACGCAAAATTCGTACCCGCAACAGTGCATA 960  
QY 1250 TGAACAAGATGAGAGAGAGAGATTTCTGGTGGCTGCAATTTTGGACTTTTGCACAAAGACG 1309  
Db 961 TGAACAAACTGGATAGAGAGAGACCTTTACAGACATTCAGTATTTTCGACAAAGGACA 1020  
QY 1310 GAAGCGGTTATATCAACCATCGATGAGCTTCAGTCACTGTTGCACAGAGTTTGGTCTATGTG 1369  
Db 1021 ACAGCGGTTACATTACTTAAAGAAGAGCTTGAGCAGCCCTTGAAGGAGCAAGGTTGTATG 1080  
QY 1370 ATACACCT---CTGGAGCAGCATGATCAAGGAGATGATTTGCACAAATGACGGGAAGATCG 1426  
Db 1081 ACGCGATAAATCAAGACATCATCTCCGATGCCGACTCTGCACATGATGGAAGATAG 1140  
QY 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAAGGAGATGAGTTGGGAGAGCAAGAACCA 1486  
Db 1141 ATTATTCAAGTTTGTGGCATGATGAGGAAGGGAGCGCTGGTCCGAGCCATGAACA 1200  
QY 1487 TGATGAAGA 1495  
Db 1201 TCAAGAAGA 1209

RESULT 2  
US-08-459-448A-20  
Sequence 20, Application US/08459448A  
Patent No. 5859336  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lytle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1226  
OTHER INFORMATION: /note= "cDNA sequence for maize  
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as  
OTHER INFORMATION: disclosed in Figure 30."  
US-08-459-448A-20

Query Match 24.6%; Score 429.8; DB 2; Length 1349;  
Best Local Similarity 60.3%; Pred. No. 1.4e-99;  
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;  
QY 290 TTGAGATCATGTCATCTCTGAGATCCAAATGTTGTAGGATCAAGGGAGCTTATG 349  
DB 1 TGGAGATCATGTCACCACTCTCGGCGAGCCCAAGCTGTGGGCTCCGCGCGGTACG 60  
QY 350 AAGATTCGGTGTGTTTCATATTTGTTAGAGGTTTGTGAAGTGTGAGCTTTTGTATC 409  
DB 61 AGGACAGCAGAGCGGTGACCTCTCATGAGCTGTGCGCGCGGGAGCTTTTCGACC 120  
QY 410 GGATGTTTCTAAAGGTCATTTAGTGAGGTCGAAGCTGTCAGCTTATTAAGAGGATTC 469  
DB 121 GCATCATGCGCGGGCGAGTACAGGAGCGCGCGCGGAGCTGCTCGCGCCATCG 180  
QY 470 TTGGTGTGTAGGCTGTGTCATTTCTTGGTGTATGATAGATCTCAAACTCTGAGA 529  
DB 181 TGCAGATCGTGCACACCTGCCACTCCATGGGGGTGATGCACCGGGACATCAAGCCCGAGA 240  
QY 530 ATTTCTGTTGTAGTCTTAAGATGATCTAAGCTTAAGGCTACCGATTGTTGTTCT 589  
DB 241 ACTTCTGCTGCTCAGCAGGACGAGCGCGGCTCAAGGCCACGACTTCGCGCTCT 300  
QY 590 CTGTCTTCTATAAGCCAGGACAATATTTATGACGAGTGTGAAGTCCGCTACTATGTTG 649  
DB 301 CGGTCTTCTCAAGAGGCGGAGCTGCTCAGGACATCGTCCGCGAGCGCTACTACATCG 360  
QY 650 CACGAGGCTCTAAGAAATGTTATGACCTGAAATAGATGTGTGAGTGTGCTGGTGA 709  
DB 361 CGCCGAGGCTCTCAAGAGGAAGTACGCGCGCGGAGCGGACATCTGGAGCGTGGGCTCA 420  
QY 710 TCCTCTCATATTTACTCAGCGGTGTCTCTCCCTCTGCGGAGAGATGAGTCTGGAATCT 769  
DB 421 TGCTCTCATCTTCTCTCGCGCGGTGCTCTCTCTCTGCGGAGAGACGAGACGCGCATCT 480  
QY 770 TTAGACAGATTTGACAGGAGTTAGATTTCAATCTGACCGGTGCTCTACTCTCAG 829  
DB 481 TCACCGCCATCTCGGAGGCGAGCTTGACCTCTCCAGCGAGCCATGGCCACATCTCGC 540  
QY 830 AAGCTGCTAAAGATTTGATCTATAAAATGCTCGAAAGAGCGCCCAAGAAACGCAATTCG 889  
DB 541 CGGAGCCAGGATCTCGTCAGAGAGATGCTCAACATCAACCCCAAGAGCGGCTCAOGG 660

QY 890 CTCATGAAGCCTTGTTGTCACCCATGCGATTTGCGATGAACAAGCAGCAGCAGCAAGCCTC 949  
DB 601 CGTTCAGGTCTCTCAATCACCCTATGATCAAGAAGCAGGAGCGCGCTTGACACGCGCG 660  
QY 950 TTGATCCAGCAGTCTTATCTCTGCTTAAGCAGTTTCTCAATGAATAAGATTAAAGAAA 1009  
DB 661 TTGACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCCATGAACCACTTCAAGAAAG 720  
QY 1010 TGGCATTACGGGTAACTGCTGAGAGACTTTTCAGAGGAGAAATTTGGAGGTCTGAAGGAAT 1069  
DB 721 CAGCATTTGAGGATCATAGCTGGTGCCTATCCGAAGAGGAGATCACAGGCTGAAGGAGA 780  
QY 1070 TGTTCAGATGATGACACAGACAGCAGCGGAAGATTACTTTTGAAGAGCTCAAGCGG 1129  
DB 781 TGTTCAGAAGCAATTCACAAGGATAACAGCGGACCATTTACCCTCGACGAGCTCAACACG 840  
QY 1130 GTTTGAAGAGAGTGGATCTGAATCTGATGGAATCAGAAATCAAGTCTCTCATGTGATCGG 1189  
DB 841 GGTGGCAAGCACGGGCCCAAGCTGTGACAGCAGGAATTCGAGAAACTAATGGAAGCAG 900  
QY 1190 CTGATATCGACAAACAGTGGTACAATAGACTACGGAGAAATTCCTAGCAGCAACCTTACACA 1249  
DB 901 CTGACGCTGACGGCAACGGGTTAATTGACTACGACGAATTCGTACCGCAACAGTGCATA 960  
QY 1250 TGAACAGATGAGAGAGAGAGAGATTTCTGTTGGTGTGATTTTCGAGCTTTTCACAAAGACG 1309  
DB 961 TGAACAAACTGGATAGAGAGAGACCTTTACAGCAGATTCAGTATTTTCGACAAAGGACA 1020  
QY 1310 GAAGCGGTTATATCACCATCGATGAGCTTCAGTCAAGTGTGCACAGAGTTGGTCTATGTG 1369  
DB 1021 ACAGCGGTGATATTACTAAAGAAGAGCTTGAGCAGCGCTTGAAGAGCAAGGTTGTATG 1080  
QY 1370 ATACACCT---CTGACAGCATGATCAAGGAGATGATCTTGAACAATGACGGGAGATCG 1426  
DB 1081 ACGCCGATAAATCAAGACATCATCTCCGATGCCGATCTGACAATGATGAAGGATAG 1140  
QY 1427 ATTTCGGAGTTTACAGCAATGATGAGAGAGGAGATGGAGTTGGGAGAGCAGAACCA 1486  
DB 1141 ATTATTCAGATTGTTGGGATGATGAGMAAGGAGCGCTGGTCCGAGCCCAATGAACA 1200  
QY 1487 TGATGAAGA 1495  
DB 1201 TCAAGAAGA 1209

RESULT 3  
US-08-459-595A-20  
Sequence 20, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Kozielec, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Surtie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005

CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,595A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1226  
OTHER INFORMATION: /note= "cDNA sequence for maize  
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as  
OTHER INFORMATION: disclosed in Figure 30."

US-08-459-595A-20

Query Match 24.68; Score 429.8; DB 3; Length 1349;  
Best Local Similarity 60.34; Pred. No. 1.4e-39;  
Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 290 TTCAGATCATGCATCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAAAGGACTTATG 349  
DB 1 TGCAGATCATGCACCATCTCTCCGGCCAGCCCAACGTTGGTGGGCTCCGGGGCGGTACG 60

QY 350 AAGATTCGGTGTGTTGTTTCATATGTTATGAGGTTTGTGAAGGTGTGAGCTTTTGTATC 409  
DB 61 AGGACAAGCAGAGCGTGCACTCTGTCATGAGCTGTGCGGGCGGGGAGCTCTTCGACC 120

QY 410 GGATTTGTTTAAAGTTCATTTTATGAGCGTGAAGCTGTCAAGCTTTATTAAGCAATTC 469  
DB 121 GCATCATCGCCGGGGCCAGTACAGCGAGCGCGCGCGCGGAGCTCTCGCGCCATCG 180

QY 470 TGGTGTGTTGAGCTGTGATCTCTCTGTTATGATGATGATGATGATGATGATGATGATG 529  
DB 181 TGCAGATCGTGACACCTGCCACCTCCATCGGGGGTGTGACCGGGGATCAAGCCCGAGA 240

QY 530 ATTCTGTGTTTATAGTCTTAAAGATGATGCTAAGCTTAAGCTTACCGATTGTTGTTGT 589  
DB 241 ACTTCTGTCTGTCAGAGGACGAGAGCGCGCGCTCAAGCCACCGACTTCGGGCTCT 300

QY 590 CTGTCTTCTAAGCCAGGACAAATATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 649  
DB 301 CGGTCTTCTTCAAGGAGGGCGAGCTGCTCAGGGACATCGTCGGGAGCGGCTTACTACATG 360

QY 650 CACCAGAGGTGCTAAAGAAATGTTATGAGCTGAATAGATGTGTGAGTGTGAGTGTGAGTGT 709  
DB 361 CGCCCGAGGTGCTCAGAGGAAGTACGGCCCGGAGCGGACATCTGGAGCGTCCGGCTCA 420

QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 769  
DB 421 TGTCTTACATCTTCTCTCGCGCGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480

QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAATCTGACCCCTGACCTACTACTCTCAG 829  
DB 481 TCACCGCCATCTCTCGAGGGCAGCTTGACCTCTCCAGCGAGCCATGCCACACATCTCGC 540

QY 830 AAGCTGCTAAAGATTGATCTATAAATGCTCGAAGAGAGCCCAAGAAAGCAATTTCTG 889  
DB 541 CGGAGCCCAAGATCTCTGCAAGAAAGTGTCTCAACATCAACCCCAAGAGCGGCTCAGG 600

QY 890 CTCTAAGACCTTGTCTCACCCTATGATGATGATGATGATGATGATGATGATGATGATG 949  
DB 601 CGTTCAGGTCTCTCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 660

QY 950 TTGATCCAGAGCTTTATCT 1009  
DB 661 TTGACAAACGTTGTTCTCGACAGGCTCAAGCGAGTTTCAGGGCCATGAACCGTTCAAGAA 720

QY 1010 TGGCATTACGGGTAAATTGCTGAGAGACTTTCAGAGGAAGAAATTTGGAGGTCTGAAGGA 1069  
DB 721 CAGCATTTAGGATCATAGCTGGGTGCTTATCGAAGAGAGATCAACAGGGCTGAAGGAGA 780

QY 1070 TGTTCAGATGATAGACACAGCAACAGCGGAAACGATTACTTTTGAAGAGCTCAAGCGG 1129  
DB 781 TGTTCAGAAACATTTGCAAGGATAACAGCGGAGCCATTACCCCTCGACGAGCTCAACAC 840

QY 1130 GTTTGAAGAGAGTCGGATCTGAATCTGATGGAATCAGAAATCAAGTCTCTCATGGATGCG 1189  
DB 841 GGTTCGAAGACAGCGGCCCAAGCTGTACAGCAGCGAAATGGAGAACTAATGGAAGCAG 900

QY 1190 CTGATATCGACAAACAGTGTGTAACAATAGACTACGGAAGATTCTTACAGCAACCTTACACA 1249  
DB 901 CTGACGCTGACCGCAACGGGTTAAATGACTACGAGCAATTCGTCAACCGCAACAGTGCATA 960

QY 1310 GAAGCGTTATATCACCATCGATGAGCTTCAGTACGTTTCAGTACGTTTCAGTACGTTTCAG 1369  
DB 1021 ACAGCGGTACATTTACTTAAAGAGAGCTTGACAGCGCTTGAAGGAGCAAGGTTGTATG 1080

QY 1370 ATACACT---CTGGAGCAGCATGATCAAGGAGTTGATCTTGACAAATGACGGAAGATCG 1426  
DB 1081 ACAGCGATAAAATCAAGAGACATCTCCGATGCCGACTCTGACAAATGATGGAAGATAG 1140

QY 1427 ATTTCTCGAGTTTACAGCAATGATGAGGAAGGAGATGAGTTGGGAGAAAGCAAGCAACA 1486  
DB 1141 ATTATTACAGATTTGTGGCGATGATGAGGAAGGAGCGGCTGTTCCGAGCAATGAACA 1200

QY 1487 TGATGAAGA 1495  
DB 1201 TCAAGAAGA 1209

RESULT 4  
US-08-459-504B-20  
; Sequence 20, Application US/084595045  
; Patent No. 6075185  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 607518artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA: US 08/459,595  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:

NAME: Melrose, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CG1577/CIP/DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

US-08-459-504B-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;

Best Local Similarity 60.3%; Pred. No. 1.4e-99;

Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

290 TTGAGATCATGTCATCTCTCTGAGCATCCAAATGTTGTAGGATCAAGGACTTATG 349

1 TGCAGATCATGACCACCTCTCGGCCAGCCCAACGTTGGGCGCTCCGCGGGGTACG 60

350 AAGATTCGGTGTGTTGTTTCAATGTTATGAGGTTTGTGAAGGTGTGAGCTTTTGTATC 409

61 AGGCAAGACAGAGGTGCACCTCTCATGAGCTGTGCGCGGGCGGGAGCTCTTCGACC 120

410 GGATGTTTCTAAAGTCATTTAGTCAGCGTGAAGCTGTCAAGCTTATTAACAGCATTC 469

121 GCATCATGCCCGGGGGCGAGTACACGAGCGCGGGCGGGAGCTGCTCGCGGCATCG 180

470 TTGGTGTGTTGAGGCTTGTCATCTCTTGGTGTGTTATGATAGAGATCTCAAACTGAGA 529

DB 181 TGCAGATCGTGCACACCTGCCACTCCATGGGGGTGATGACCCGGGACATCAAGCCCGAGA 240  
QY 530 ATTTCTGTTTGTATAGTCTCTAAAGATGATCTAAGCTTAAAGGCTACCGATTTTGGTTGT 589  
DB 241 ACTTCCTGCTCTCAGCAAGACGAGGACGGCGCTCAAGGCCACCGACTTCGGCTCT 300  
QY 590 CTGCTCTTATAAGCCAGGACAATTTATATGACGTAGTTGAAGTCCGTACTATGTTG 649  
DB 301 CCGTCTTCTCAAGGAGGGGAGTGTCTCAGGGACATCGTCGCGAGCGCTACTCATCG 360  
QY 650 CACCAAGGTGCTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGAGTGTCTGGTGT 709  
DB 361 CCGCCGAGGTGCTCAAGAGGAGTACGGCCGGAGGCGGACATCTGGAGCGTGGGCTCA 420  
QY 710 TCCCTACATTTTACTCAGCGGTGTTCTCCCTTCTGGGAGAGACTGAGTCTGGATCT 769  
DB 421 TGCTCTACATCTTCTCCCGCGCTGCTCTCCCTTCTGGGAGAGAACGAGACGGCATCT 480  
QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCTTACTATCTCAG 829  
DB 481 TCACCGCATCTCTGGAGGCGAGCTTGACCTCTCCAGGAGCCATGGCCACACATCTCGC 540  
QY 830 AAGCTGCTAAAGATTGATCTATAAAATGCTCGAAAGAGCGCCCAAGAAACGCAATTTCTG 889  
DB 541 CGGGAGCCAAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGCTCACGG 600  
QY 890 CTCATGAAGCTTGTGTCAACCCATGATGTCGATGAACAGACAGACAGACAGCAAGCTC 949  
DB 601 CGTTCAGGTCTCTCAATCACCCATGATCAAGAGAGCGGAGACGCGCTTGACACGCGC 660  
QY 950 TTGATCCAGCAGTCTTATCTCTCTTAAAGCAGTTTCTCAAAATGAATAAGATTAAAGAAA 1009  
DB 661 TTGACAAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCCATGAACAGTTCAAGAAAG 720  
QY 1010 TGGCATTACGGTAATTCCTGAGAGACTTTCAGAGGAGAAATTTGGAGTCTGAAGGAAT 1069  
DB 721 CAGCATTTAGGATCATAGCTGGTGCCTTATCCGAAGAGGATCACAGGGCTGAAGGAGA 780  
QY 1070 TGTTCAGATGATAGACACAGACAAACAGCGGAACGATTACTTTTGAAGAGCTCAAGCGG 1129  
DB 781 TGTTCAAGAACATTGCAAGGATAACAGCGGACCATTTACCTCGACGAGCTCAACACAG 840  
QY 1130 GTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCTCATGGATCGG 1189  
DB 841 GGTTCGCAAGCAGCGGCCCAAGCTGTCCAGACGCGAAATCGAGAAACTAATGGAAGCAG 900  
QY 1190 CTGATATCGACAACAGTGTGTACATAGACTACGGAGAATTCCTAGCAGCAACCTTACACA 1249  
DB 901 CTGACGCTGACCGCAACGGTTAATTGACTACGAGATTCGTCAACCGCAACAGTGCATA 960  
QY 1250 TGAACAAGATGAGAGAGAGGAGATTCTGGTGGCTGCAATTTTCGAGCTTTTGACAAAGACG 1309  
DB 961 TGAACAAACTGGATAGAGAAGACACCTTTACACAGCATTCAGTATTTTCGACAAAGGACA 1020  
QY 1310 GAGCGGTTATATCACCATCGATGAGCTTCAGTCAGTTGACAGAGTTTGGTCTATCTG 1369  
DB 1021 ACAGCGGTGACATTAATAAGAGAGCTTTGACGCGCTTGAAGGAGCAAGGGTTGATG 1080  
QY 1370 ATACACT...CTGGACGACATGATCAAGGAGATTGATCTTGAACAATCAGCGGAGATCG 1426  
DB 1081 ACGCCGATAAATCAAGACATCATCTCCGATGCCGCTCTGACAAATGATGGAAGGATAG 1140  
QY 1427 ATTTCTCGGAGTTTACAGCAATGATCAGGAAGGAGATGGAGTTGGGAGAGACGAAACA 1486  
DB 1141 ATTATTACAGATTGTTGGCGATGATGAGAAAGGACCGCTGGTCCGAGCCATGAACA 1200  
QY 1487 TGATGAAGA 1495  
DB 1201 TCAGAAGA 1209

RESULT 5

US-08-459-444-20

Sequence 0, Application US/08459444A

Parent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 1054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/Pl/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8597

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note= "cdna sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEetical: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-08-459-444-20

Query Match 24.6%; Score 429.8; DB 3; Length 1349;

Best Local Similarity 60.3%; Pred. No. 1.4e-99;

Matches 729; Conservative 0; Mismatches 477; Indels 3; Gaps 1;

QY 290 TTCAGATCATGATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGAGTTATG 349

DB 1 TGCAGATCATGACCACTCTCCGGCCAGCCCAACGTGTGTGGCCCTCCGGCGCGGTACG 60

QY 350 AAGATTGGTGTGTTTCATATGTTATGGAGTTGTGAAGTGTGTGTTTGTATC 409

DB 61 AGGCAAGCAGAGCGTGCACCTCTCATGGAGCTGTGCCGGCGGGAGCTCTTCGACC 120

QY 410 GGATTGTTTCTTAAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTTATTAAGAGATTTC 469

DB 121 GCATCATCGCCCGGGCCAGTACACGAGCGCGCGCGGAGCTGTCTGCGGCGCATCG 180

QY 470 TTGTTGTTGTTGAGGTTGTCATTCCTTTGTTGTTATGATGATAGATCTCAAACTGAGA 529

DB 181 TGCAGATCGTGCACACCTGCTCCATCGGGGTGATGACCCGGGACATCAAGCCCGAGA 240

QY 530 ATTTCCTTTGTTGATAGTCTTAAAGATGATGCTAAAGTAAAGCTACCGATTTTGGTTGT 589

DB 241 ACTTCCTGCTCTCAGCAAGGACGAGACGCGCCCTCAAGGCCACCGACTTCGGCTCT 300

QY 590 CTGCTCTCTATAAGCCAGACACAATATTTATGACGTAGTTGGAAAGTCCGTACTATGTTG 649

DB 301 CCGTCTCTCTCAAGGAGGCGAGCTCTCAGGACATCGTCGGCAGCGCTACTACTACATCG 360

QY 650 CACCAGAGGTGCTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGAGTCTGTGTGTTA 709

DB 361 CGCCGAGGTGCTCAAGAGGAGTACGCGCCCGAGGCGGACATCTGGAGCGTCGCGCTCA 420

QY 710 TCCTCTACATTTTACTCAGCGGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 769

DB 421 TGCTCTACATCT 480

QY 770 TTAGACAGATATTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCTACTATCTCAG 829

DB 481 TCACCGGCATCTCTCGAGGCGAGCTTGACCTCTCCAGCGAGCCATGGCCACACATCTCG 540

QY 830 AAGTGTCTAAAGATTGATCTATAAATGCTCGAAGAGAGCCCGAAGAAAGCATTTCTG 889

DB 541 CGGAGGCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGTCTACGG 600

QY 890 CTCATGAAGCCTTGTGTCAACCATGATGATGATGATGATGATGATGATGATGATGATG 949

DB 601 CGTTCAGGTCTCTCAATCACTCCATGATCAAAAGAGACGAGACGCGCTGACACGCGC 660

QY 950 TTGATCAGCAGCTTTATCTCTGCTTAAAGCAGTTTCTCAATGATGATGATGATGATG 1009

DB 661 TTGCAACAGTTGTTCTCGACAGGCTCAAGCAGTTTCAAGGCGCATGAACAGTTCAG 720

QY 1010 TGGCATTACGGTAAATGCTGAGAGACTTTCAGAGAGAGAAATTTGAGGCTCTGAAGGA 1069

DB 721 CAGCATTTGAGGATCATAGCTGGGTGCTTATCGAAGAGGAGATCACAGGGCTGAAGG 780

QY 1070 TGTTCAGATGATAGACACAGACAGCGGAGACGATTTTTCAGAGAGCTCAAGCGG 1129

DB 781 TGTTCAGAAACATTTGACAGGATTAACAGCGGACCATTTACCTCGACGAGCTCAAC 840

QY 1130 GTTTGAAGAGAGTCTGGATCTGAACTGATGGAATCAAGATCAAGATCTCTCATGGATCG 1189

DB 841 GGTTCGCAAGACGCGGCCCAAGCTGTGACAGCGAAATGGAGAAACTAATGGAAGCAG 900

QY 1190 CTGATATCGCAACAGTGTGTACATAGACTAGGAGATTTCTAGCAGCAGCACTTACACA 1249

DB 901 CTGACGCTGACGCAACGGTTAAATGACTAGCAGAAATTCCTACCCGCAACAGTGCATA 960

QY 1250 TGAACAAGATGGAGAGAGAGGATTTCTGTGGCTGCAATTTTCGGACTTTGACAAAGAC 1309

DB 961 TGAACAACCTGGATAGAGAGAGACCTTTTACACAGCATTTCCAGTATTTTCGACAAAG 1020

QY 1310 GAAGGGTTATATCACCATCGATGAGCTTCACTCAGCTGACAGAGTTTGGTCTATGTC 1369

DB 1021 ACAGCGGTATATCTTAAAGAGAGCTTGACAGCGCTTTGAGGAGCAAGGTTGTATG 1080

QY 1370 ATACACCT---CTGGACGACATGATCAAGGAGATTGATCTTGACAAATGACGGGAGATCG 1426

DB 1081 ACGCCGATAAATCAAAAGACATCATCTCCGATGCCGACTCTGACAAATGATGAAGATAG 1140

QY 1427 ATTTCTCGGCTTTACAGCAATGATGAGGAGAGATGAGATGAGTGTGGAGAGAGCAACCA 1486

DB 1141 ATTATTCAGAGTTTGTGGCATGATGAGGAAAGGAGCGCTGGTCCGAGCAATGAAACA 1200

QY 1487 TGAAGAAGA 1495



Db 1081 ACGCGGATAAAATCAAGACATCATCTCCGATGCCGACTCTGCAATGATGGAAGGATAG 1140  
QY 1427 ATTTCGAGTTTACACCATGATGAGGAAGGAGATGGAGTTGGAGAAGCAGAACCA 1486  
Db 1141 ATTATTCAGAGTTTGTGGCGATGATGAGGAAGGAGCGGTGTGGCGGACCAATGAACA 1200  
QY 1487 TGATGAAGA 1495  
Db 1201 TCAAGAAGA 1209

RESULT 7  
US-08-459-448A-26  
; Sequence 26, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothelein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5859336attis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; STREET: Rd. POB 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,448A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40403  
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8582  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4162 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO

FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1418..1427  
OTHER INFORMATION: /note= "start of mRNA"  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1481..2366  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2367..2451  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2452..2602  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2603..2690  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2691..2804  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2805..2906  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2907..3075  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3076..3177  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3178..3304  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3305..3398  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3399..3498  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3499..3713  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3714..3811  
FEATURE:  
NAME/KEY: promoter  
LOCATION: 1..1477  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /partial  
OTHER INFORMATION: /function= "pollen-specific promoter region"  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
US-08-459-448A-26  
Query Match 12.5%; Score 218; DB 2; Length 4162;  
Best Local Similarity 59.8%; Pred. No. 9.4e-46;  
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;  
QY 142 TACCITCTGGGAAAAGCTAGGCCAAGCCAAATTGGAAACAACCTATCTCTGCACAGAG 201  
Db 1757 TACTCATGGCAAGAGCTCGGGCGGGGAGTTCGCGTGACGCACCTGTGCACGCAC 1816  
QY 202 AAATCAACCTCCGCTAATTACCGCTCGCAAAATCGATCCGGAAGCGAAAGCTCGTGTGCG 261  
Db 1817 CGGACGAGCGGCGAGAGCTGGCGTCAAGACAGCATCGGGAAGCGGAAGCTCGCGCCAGG 1876  
QY 262 GAGGATTAGAGATGATGGCGTGAGATTCAGATCATGATCATCTCTGTGAGATCCA 321  
Db 1877 GAGGAGTGGACGACGTGGCGGGAGGTGCAGATCATGCACCTCTCCGGCCAGCCC 1936  
QY 322 AATGTTGTTAGGATCAAGGGGACTTATGAAGATTGCGTGTGTTGTTTCATATTGTTATGGAG 381  
Db 1937 AACGTGTTGGGCTCCGCGCGCGTACGAGGACAAGAGCGGTGCACCTCGTCATGGAG 1996  
QY 382 GTTTGTGAAGGTGGTGAAGCTTTTGTGATCGGATGTTTCTAAAGGTCAATTTAGTGAGCGT 441

Db 1997 CTGTGCGCGCGGAGCTCTTCGACCGCATCATCCCGGGGCCAGTACACGGAGCGC 2056  
Qy 442 GAAGCTGTCAAGCTTATTAAAGACCATCTTGGTGTGTTGAGGCTTGTCTATCTCTTTGTT 501  
Db 2057 GCGCGCGGAGCTGCTGGCGGCATCGTGCAGATCGTGACACCTGCCACTCCATGGGG 2116  
Qy 502 GTTATGATAGATATCTCAACACCTGAGAAATTTCTTGTGATAGTCTTAAGATGATGCT 561  
Db 2117 GTGATGACCGCGGACATCAACCGCGAAGTCTCTGCTGCTCAGCAAGGACGAGGACGG 2176  
Qy 562 AAGCTTAAGGCTACCGATTTTGGTGTGTTGCTCTCTATAAGCCAGACATAATTTATAT 621  
Db 2177 CCGCTCAAGGCCACCGATCTCGGCTCTCCGCTCTCTTCAAGGAGCGAGTGTCTCAGG 2236  
Qy 622 GACGTAGTTGAAGTCCGTACTATGTTGACCCAGAGTGTCTAAAGAAATTTATGACCT 681  
Db 2237 GACATCGTCGCGAGCGCTACTACATCGGCGCGAGTGTCTCAAGAGAAAGTACGCGCCG 2296  
Qy 682 GAATAGATGTGTGAGTGTGGTGTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCC 741  
Db 2297 GAGCGGACATCTGGAGCTGCGGCTGATGCTCTACATCTTCTCGCGCGGTGCTCTCC 2356  
Qy 742 TTCTGGGCGAG 751  
Db 2357 TTCTGGGCGAG 2366

RESULT 8

US-08-459-595A-26  
; Sequence 26, Application US/08459595A  
; Patent No. 6018104  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6018104artis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; STREET: Rd., POB 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,595A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4162 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1418..1427  
OTHER INFORMATION: /note= "start of mRNA"  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1481..2366  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2367..2451  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2452..2602  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2603..2690  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2691..2804  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2805..2906  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2907..3075  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3076..3177  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3178..3304  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3305..3398  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3399..3498  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3499..3713  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3714..3811  
FEATURE:  
NAME/KEY: promoter  
LOCATION: 1..1477  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /partial  
OTHER INFORMATION: /function= "pollen-specific promoter region"  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
US-08-459-595A-26

Query Match 12.5%; Score 218; DB 3; Length 4162;  
Best Local Similarity 59.8%; Pred. No. 9, 4e-46;  
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 142 TACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGACAACTATCTCTGCACAG 201  
Db 1757 TACTCGATGGGCAAGGAGCTCGGCGCGGGCAGTTCGGCGTGACGACCTGTGCGACGCAC 1816  
QY 202 AAATCAACCTCCGCTAATTACGCTCGCAATCGATCCGGAAGCGAAAGCTCGTGTGTCGC 261  
Db 1817 CGGACGAGCGCGAGAGCTGGCGTCAAGACGATCCGGAAGCGAAGCTGGCGGCGCAGG 1876  
QY 262 GAGGATTACGAAGATGTATGTCGCTGAGATTGAGATCATGTCATCATCTCTCTGAGCATCCA 321  
Db 1877 GAGGACGTGGACGAGCTGCGCGCGGGAGGTGCAGATCATGCACCACTCTCTCGGCCACGCC 1936  
QY 322 AATGTTGTAGATCAAGGACCTTATGAAGATTCGCTGTTTGTATATGTTATGAGG 381  
Db 1937 AACGTGGTGGGCGCTCGCGCGCGCGTACGAGCAAGCAGAGCGGTGCACCTCGTCATGGAG 1996  
QY 382 GTTCTGGAAGTGTGAGCTTTTGTATCGGATTTCTTAAAGTCAATTTTATGAGCGT 441  
Db 1997 CTGTGCGCGCGGGGAGCTCTTCGACCGCATCATCGCCGGGCGCAGTACAGGAGCGC 2056  
QY 442 GAAGCTGTCAAGCTTATTAAGACGATTCCTGCTGTTGAGGCTTGTGCTTCTCTTGGT 501  
Db 2057 GCGCGCGCGGAGCTCTCGCGCGCATCTGTGAGATCGTGACACCTCCCACTCATGCGGG 2116  
QY 502 GTTATGCTAGAGATCTCAAACTCAGAAATTTCTTTTGTATAGTCTCTAAAGATGATGCT 561  
Db 2117 GTGATGCAACCGGACATCAAGCCCGGAGACTTCTGCTGCTCAGCAAGGACGAGACGG 2176  
QY 562 AAGCTTAAGCTACGATTTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 621  
Db 2177 CGGCTCAAGGCGGAGCTCTCGCGCGCTCTCGCTCTCTCTCTCTCTCTCTCTCTCTCT 2236  
QY 622 GAGCTAGTTGGAGTCCGCTACTATGTTGACCAAGAGTGTCTAAAGAAATGTTATGGACCT 681  
Db 2237 GACATCGTCCGAGCGCTACTACTATCGCGCGCGGAGTGTCTCAAGAGGAAGTACGCGCG 2296  
QY 682 GAAATAGATGTGTGAGAGTCTCGTGTATCTCTCTACATTTTACTCAGCGGTGTTCTCCC 741  
Db 2297 GAGGCGGACATCTGGAGCTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2356  
QY 742 TTCTGGGCGAG 751  
Db 2357 TTCTGGGCGAG 2366

RESULT 9

US-08-459-504B-26

Sequence 26 Application US/08459504B

Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttle, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8887

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 4162 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1418..1427

OTHER INFORMATION: /note= "start of mRNA"

FEATURE:

NAME/KEY: exon

LOCATION: 1481..2366

FEATURE:

NAME/KEY: intron

LOCATION: 2367..2451

FEATURE:

NAME/KEY: exon

LOCATION: 2452..2602

FEATURE:

NAME/KEY: intron

LOCATION: 2603..2690

FEATURE:

NAME/KEY: exon

LOCATION: 2691..2804

FEATURE:

NAME/KEY: intron

LOCATION: 2805..2906

FEATURE:

NAME/KEY: exon

LOCATION: 2907..3075

FEATURE:

NAME/KEY: intron

LOCATION: 3076..3177

FEATURE:

NAME/KEY: exon

LOCATION: 3178..3304

FEATURE:

NAME/KEY: intron

LOCATION: 3305..3398

FEATURE:

NAME/KEY: exon

LOCATION: 3399..3498

FEATURE:

NAME/KEY: intron  
LOCATION: 3499..3713  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3714..3811  
US-08-459-504B-26

Query Match 12.5%; Score 218; DB 3; Length 4162;  
Best Local Similarity 59.8%; Pred. No. 9.4e-46;  
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 142 TACCTTCTGGAAAAAGCTGAGCCAAAGCCAAATTTGGAAACAACTATCTCTGCACAGAG 201  
Db 1757 TACTCGATGGGCAAGAGCTCGGCGCGGCGAGTTCGGGCTGACGACCTGTGACGAC 1816  
QY 202 AATCAACCTCCGCTAATTAACGCTCCGAATCGATCCGAAAGCGAAAGCTCGTGTGCGC 261  
Db 1817 CGGACGAGCGCGGAGAGCTGGCGTCCAGACGATCCGAAAGCGAAAGCTGGCGCCAGG 1876  
QY 262 GAGGATTACGAAGATGTATGGCTGAGATTTCAGATCATCATCTCTCTGAGATCCA 321  
Db 1877 GAGGACGTGACGACGTGCGCGGGAGGTGCAGATCATGCACACCTCTCCGGCCAGCCC 1936  
QY 322 AATGTTTATAGGATCAAGGACTTATGAGATTCGGTGTGTTTCATATCTTTATGGAG 381  
Db 1937 AACGTGTGGGCTCCGCGCGGCTACGAGGACAGAGCGTGACCTGCACTCATGTGAG 1996  
QY 382 GTTGTGAAGTGTGAGCTTTTGTATCGGATTTTCTTAAAGGTCAITTTTGTAGCGGT 441  
Db 1997 CTGTGCGCGGGGGAGCTCTTCGACCGCATCATCGCCGGGCGAGTACACGAGCGC 2056  
QY 442 GAGCTGTCAAGCTTATTAAGAGATCTTGTGTTGTTGAGGCTGTGATCTCTTTGTT 501  
Db 2057 GGCCTCGCGGAGCTGTGCGCGGCTGTCAGATCTGTCAGATCTGTCACACCTGCCATCGGG 2116  
QY 502 GTTATGATAGATCTCAAACTGAGATTCTTGTGTTGATGCTCTAAAGATGATGT 561  
Db 2117 GTGATGACCGGACATCAAGCCGAGACTTCTGCTGCTCAGCAAGGACGAGCGG 2176  
QY 562 AAGCTTAAGCTACCGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 621  
Db 2177 CCGCTCAAGGCCACCGACTTCGGGCTCTCGCTCTTCTTCAAGGAGGCGAGCTGCTCAGG 2236  
QY 622 GACCTAGTGGAGTCCGTAATGTTGTCACGAGAGTGTCTAAAGAAATGTTATGACCT 681  
Db 2237 GACATCTGCGGACGCTACTACATCGCCCGAGTGTCTAAGAGGAAGTACGCGCG 2296  
QY 682 GAAATAGATGTGTGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCC 741  
Db 2297 GAGCGCGACATCTGAGCGTGGCGTCTATGCTCTACATCTTCTCGCGGCGTCTCC 2356  
QY 742 TTCTGGCGAG 751  
Db 2357 TTCTGGCGAG 2366

RESULT 10  
US-08-459-444-26  
Sequence.26, Application US/08459444A  
Patent No. 6121014  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.  
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459.444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/SOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4162 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1418..1427  
OTHER INFORMATION: /note= "start of mRNA"  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1481..2366  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2367..2451  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2452..2602  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2603..2690  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2691..2804  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2805..2906  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2907..3075  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3076..3177  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3178..3304  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3305..3398  
FEATURE:  
NAME/KEY: exon

Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/547,422  
APPLICATION NUMBER: US/09/547,422  
FILING DATE: 11-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8567  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4162 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1418..1427  
OTHER INFORMATION: /note= "start of mRNA"  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1481..2366  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2367..2451  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2452..2602  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2603..2690  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2691..2804  
FEATURE:  
NAME/KEY: intron  
LOCATION: 2805..2906  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2907..3075  
FEATURE:  
NAME/KEY: intron  
LOCATION: 3076..3177  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3178..3304

Query Match 12.5% Score 218; DB 3; Length 4162;  
Best Local Similarity 59.8%; Pred. No. 9 4e-46;  
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;  
QY 142 TACCTTTGGGAAAAGACTAGGCGAAGGCCAATTTGGACACACCTATCTCTCCACAGAG 201  
DB 1757 TACTCGATGGGCAAGGAGCTCGGCGGGGAGTTCGGCGTGACGACCTGTGCGACGAC 1816  
QY 202 AAATCAACTCGCTAATTACGCTGCAAAATCGATCCGGAAGCGAAAGCTCGTGTGCGC 261  
DB 1817 CGACGACGGGGAGAACTGGGTGCGAGACGATCGGAAAGCGGAAGCTGGCGGCCAGG 1876  
QY 262 GAGGATTACGAGATGATGGCGTGAGATTGAGATCATGATCATCTCTCTGAGCATCCA 321  
DB 1877 GAGGACGTGGACACGTGCGGCGGGAGGTGAGATCATGACCACTCTCTCGGCCAGCCC 1936  
QY 322 AATGTGTAGATCAAGGAGACTTATGAAGATTCGGTGTGTTGTCATATTGTTATGGAG 381  
DB 1937 AACGTGGTGGGCTCCGCGGCGCGTACGAGGACAGACGACGTCGACCTCGTCATGGAG 1996  
QY 382 GTTGTGAAGTGTGAGCTTTTGTATCGGATTTGTTCTAAAGTCTATTTTATGAGCGGT 441  
DB 1997 CTGTGCGGCGGGGAGGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACCGGAGCG 2056  
QY 442 GAAGTCGCAACTTATTAGACGATTTCTGGTGTGTTGAGGCTTGTCATCTCTCTGTT 501  
DB 2057 GCGCGCGGAGAGCTGCTGCGCGCCATGCTGAGATCGTGACACCTGCCACTCATGGGG 2116  
QY 502 GTATGATAGATGATCTCAAACTGAGAAATTTCTTTGTTGATGCTCTTAAAGATGATGCT 561  
DB 2117 GTATGACCCGGGACATCAAGCCGAGAACTTCCTGCTGCTCAGAGGACGAGGAGCGG 2176  
QY 562 AAGCTTAAGGCTACCGATTTGGTTGTTGCTCTCTCTATAGCCAGGACATATTATAT 621  
DB 2177 CGCTCAAGGCCACCGACTTCGCGCTCTCCGCTCTCTTCTTCAAGGAGGCGGAGCTCTCAGG 2236  
QY 622 GAGCTAGTTGGAAGTCCGTAATGTTGACAGAGGTGCTAAAGAAATGTTATGACCT 681  
DB 2237 GATCGTGGCAGCCCTACTACATCGCGCCGCGAGGTGCTCAAGAGGAAGTACGGCCCG 2296  
QY 682 GAAATAGATGTGTGAGAGTCTGGTGTATCTCTATCTTACTCAGCGGTGTTCTCTCCC 741  
DB 2297 GAGGCCGACATCTGGAGCGCTCGCGCTCATGCTCTACATCTTCTCTCGCGCGGTGCTCTCC 2356  
QY 742 TTCTGGGCGAG 751  
DB 2357 TTCTGGGCGAG 2366

RESULT 11  
US-09-547-422-26  
Sequence 26, Application US/09547422  
Patent No. 6320100  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.

RESULT 12  
US-07-951-715A-26  
; Sequence 26, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.

LOCATION: 2907..3074  
FEATURE: intron  
NAME/KEY: 3075..3177  
LOCATION: 3075..3177  
FEATURE: exon  
NAME/KEY: 3178..3305  
LOCATION: 3178..3305  
FEATURE: intron  
NAME/KEY: 3306..3397  
LOCATION: 3306..3397  
FEATURE: exon  
NAME/KEY: 3398..3497  
LOCATION: 3398..3497  
FEATURE: intron  
NAME/KEY: 3498..3712  
LOCATION: 3498..3712  
FEATURE: exon  
NAME/KEY: 3713..3811  
LOCATION: 3713..3811  
US-07-951-715A-26

Query Match 12.5%; Score 218; DB 1; Length 4165;  
Best Local Similarity 59.8%; Pred. No. 9.4e-46;  
Matches 365; Conservative 0; Mismatches 245; Indels 0; Gaps 0;  
QY 142 TACCTTCTGGGAAAAGCTAGCCAAAGCCAAATTTGGAACAACCTATCTCTGCACAGAG 201  
Db 1755 TACTCGATGGGCHAGAGCTCGGGCGGGGAGTTTCGGCGTGACGCACCTGTGCACGCAC 1814  
QY 202 AATCAACCTCCGCTAATTAGCGCTGCAATCGATCCGAGCGAAGCTCGTGTCGC 261  
Db 1815 CGACGAGCGCGGAGAAGCTGGCGTGCAGACGATCGGAAGCGGAAGCTGGCGCCACG 1874  
QY 262 GAGGATTAACAGATGATGGCGTGAGATTCAGATCATCATCTCTCTGAGCATCCA 321  
Db 1875 GAGACGTGACGAGCTGGCGGGAGGTGCGATCAIGCACCACTCTCCGGCAGGCC 1934  
QY 322 AATGTTGTTAGGATCAAGGACCTTAAGAGATTCGTTGTTGTCATATGTTATGAG 381  
Db 1935 AAGCTGTGGGCTCCGGCGCGGTACGAGGACAGAGCGTGCACTCGTCATGAG 1994  
QY 382 GTTGTGAAGGTGGAGCTTTTGTGATCGATGTTTCTAAAGGTCAATTTAGTGAGCGT 441  
Db 1995 CTGTGCGGGCGGGAGCTCTTCGACCGATCATCGCCGGGGCCAGTACACGAGCGC 2054  
QY 442 GAAGCTGTCAAGCTTAATAAGACGATCTTGTGTTGTTGAGGCTTGTCAATCTCTTGT 501  
Db 2055 GGGCCCGGAGCTGCTGCGGCCATCTGTCAGATCGTGCACACCTGCCACTCCATGGG 2114  
QY 502 GTTATGATAGATCTCAACCTGAGATTTCTTGTGATAGTCTTAAAGATGATGCT 561  
Db 2115 GTGATGACCGGGACATCAAGCCGAGAACTTCTGCTGCTCAGCAAGCAGGACGCG 2174  
QY 562 AAGCTTAAGGCTACCGATTTTGGTTGTTGTTCTTCTATAAGCCAGGACAAATTTATAT 621  
Db 2175 CGCTCAAGGCCACCGACTTCGGCTCTCTCTTCAAGAGGGCGAGCTGCTCAGG 2234  
QY 622 GACGTAGTTGAAGTCGCTACTAGTTGACCGAGGTGCTAAGAAATGTTATGACCT 681  
Db 2235 GACATGCTGCGACGCGCTACTACATCGCCCGAGGTGCTCAAGAGGAAATGACGCGCG 2294  
QY 682 GAAATAGATGTTGGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCC 741  
Db 2295 GAGCGGACATCTGGAGCTGGCGGTGATGCTCTACATCTCTCTCGCGCGGTGCTCTCC 2354  
QY 742 TCTGGGCGAG 751  
Db 2355 TTCTGGGCGAG 2364

RESULT 13  
US-09-347-801-3  
Sequence 3, Application US/09347801

Patent No. 6262345  
GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
APPLICANT: Lee, Jian Ming  
TITLE OF INVENTION: Plant Protein Kinases  
FILE REFERENCE: BB-1171  
CURRENT APPLICATION NUMBER: US/09/347,801  
CURRENT FILING DATE: 1999-07-02  
EARLIER APPLICATION NUMBER: 60/092,438  
EARLIER FILING DATE: July 10, 1998  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 3  
LENGTH: 2374  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-347-801-3

Query Match 10.9%; Score 189.6; DB 4; Length 2374;  
Best Local Similarity 53.8%; Pred. No. 1.2e-38;  
Matches 440; Conservative 0; Mismatches 369; Indels 9; Gaps 2;  
QY 271 GAAGATGATGGCGTGAGATTCAGATCATCATCTCTCTGAGCATCCAAATGTTGT 330  
Db 846 GAGGATGTTCTGAGAGTAAATTTTGAGAGCGTTATCAGGCGCAATAATCTCGTC 905  
QY 331 AGGATCAAGGAGCTTATGAAGATTCGGTGTGTTGTCATATTTGTTATGAGGTTTGTGA 390  
Db 906 AATATCTATGATGATGTGAGGATGGCTCAATGTCTACATTTGTCATGGAATTTATGTAG 965  
QY 391 GGCGTGAGCTTTTGTGCGGATTTTCTAAAGGTCAATTTTATGAGCGTGAAGCTGTC 450  
Db 966 GAGGAGAAATGCTAGACAGAAATATTAGCCAGAGCGGAGATACACAGAGGAAGATGCC 1025  
QY 451 AA---GCTTATTAAGACGATCTTGGTGTGTTGAGGCTGTCTATCTCTTGTGTTATG 507  
Db 1026 AAGCGATTTGTTGACAGATTTTGAGCGTAGTAGCTTCTGTCTATCTTCAGGGGGTAGTG 1085  
QY 508 CATAGAGATCTCAACCTCGAGATTTCTTGTGTTGATAGTCTTAAAGATGATGCTAAGCTT 567  
Db 1086 CATCGGATTTGAGCCAGAGAAATTTCTTTTCAACACGAGGATGAAATGCTCCCATG 1145  
QY 568 AAGGCTACCGATTTTGGTTGTCTGTCTTCTATAAGCCAGGACAAATTTATATGAGCTA 627  
Db 1146 AAGTTGATGATTTTGGTCTCTCTGATTTTATTAGCCAGATGAAGGCTTAATGATATT 1205  
QY 628 GTTGAAGTCCGTACTATGTGTCACGAGGCTGCTAAAGAAATGTTATGAGACCTGAAATA 687  
Db 1206 GTTGAAGTGCATATATGTTGCCCGAGAGGTTTACACAGATCATATAGTATGGAAGA 1265  
QY 688 GATGTGTGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCTCTTCTGG 747  
Db 1266 GACATTTGGAGTATAGTGTCTATAACGTACATTTCTGTCTGTGGCAGTCGGCCATCTGG 1325  
QY 748 GCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCAATCT 807  
Db 1326 GCACGAACAGAAATCAGGAATATTTCGATCTGTGTTGAGAGCTGATCCCACTTTGATGAT 1385  
QY 808 GACCGTGGCGCTACTATCTCAGAAGCTGCTAAAGATTTTATCTATAAATGCTCGAAAG 867  
Db 1386 TCACCGTGGCTACATATACGTACGTGAGCTAAGGATTTTGTGAAGAGATTTCTGAAACAA 1445  
QY 868 AGCCCCAAGAAACGCAATTTCTGCTCATGAAGCTTTGTCTACCCCATGATTTGTCGATGAA 927  
Db 1446 GATTACCGCAAAAGAAATGACCGCTGTTCAAGCACTGACTCATCTTGGTTGGAGATGAA 1505  
QY 928 CAAGCAGCACACAGAGCTCTTGATCCAGCAGCTTATCTCTGCTCTAAAGCAGTCTTCT 987  
Db 1506 CA-----AAGGCAGATCCCGCTGGACATCTCACTTCAGATTTAATTAAGCAATACCTC 1559  
QY 988 CAATGAATTAAGAAATTAAGAAATGCAATTAACGGGTAATTTGCTGAGAGACTTTTCAGAGAA 1047  
Db 1560 CGCGCTACACCTCTCTAAACGGTTGGCAATTAAGGCACTATCCAAAGGCTTTAAGGGAAGAT 1619



Fri Feb 14 09:44:26 2003

```

; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: Sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-338-057-1

Query Match          9.4%; Score 165; DB 1; Length 1400;
Best Local Similarity 54.5%; Pred. No. 1.6e-32;
Matches 330; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 313 GAGCATCCAAATGTTGTAGGATCAAGGAGCTTATGAAGATTCCGGTGTGTTTCATATT 372
   |||||
Db 151 GATCATCTAATATCATGAATATATATGAATCTTTGAGGATAAAGGATACCTTTATCTT 210
   |||||
QY 373 GTTATCGAGGTTTGTGAAGTGGTGGCTTTTGTATCGGATTGTTCTAAAGGTCATTTT 432
   |||||
Db 211 GTTACAGAAGTATATACAGGAGGAATTTTGTGAAATTTATTCGAAAAGATTC 270
   |||||
QY 433 AGTGAAGCTGAAGCTCTCAAGCTTTATTAAGACGATCTTGGTGTGTTGTAGCGCTTGTCAT 492
   |||||
Db 271 AGCGAGCGGATCGACCTCGTATAGTACGTCAAGTCTTATCGGGTATAAATATATGCAT 330
   |||||
QY 493 TCTCTTGGTGTATGATGAGATCTCAACCTGAGATTTCTTGTGATAGTCTCTAAA 552
   |||||
Db 331 CGTAATAAATAGTTCATAGAGATTTAAAGCCGAGAGATTTATTTATTAGAGAAATAAAAA 390
   |||||
QY 553 GATGATGCTAAGCTTAAGGCTACCGATTTTGGTGTGTTGTCTCTCTATATAAGCCAGGACAA 612
   |||||
Db 391 AAAGATGCAATATACGAATTATTGATTTGGGTATCTACACATTTTGAGCCCCAAAA 450
   |||||
QY 613 TATTTATAGCTAGTGTGAGTCCGTAAGTGTGTTGACACGAGTGTCTAAAGAAATGT 672
   |||||
Db 451 AAAATGAAGGATAAAATCGGACCGGCTACTACATTCGCCCTGAGGTGCTGACGGAAACA 510
   |||||
QY 673 TATGGACCTGAATAGATGTGAGTGTGTTGTGTTATCTCTACATTTTACTCAGCGGT 732
   |||||
Db 511 TACGATGAGAAATGCGACGTCTGGTCTACGGGTGTTATCTCTATATCTTCTCTGTT 570
   |||||
QY 733 GTTCCTCCCTTCTGGGAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAG 792
   |||||
Db 571 TGTCTCCATTTAACGAGCAATGAATTTGAATTTCTAAAGAAAGTCGAGAAAGGAAAA 630
   |||||
QY 793 TTAGATTTCAATCTGACCGTGGCTCTACTATCTCAGAGGCTGCTAAAGATTGATCTAT 852
   |||||
Db 631 TTACCTTCGATTTACACAGTGGCGTTAGGTTAGCGACCGCAAGATTTAATTAGG 690
   |||||
QY 853 AAAATGCTGAAAGGAGCCCAAGAAACCAATTTCTGCTCATGAAGCCCTTGTCACCCA 912
   |||||
Db 691 AAGATGTTAGCATATGTACCTCAATGCGGTATATACGAAAGAGATGCATTAGATCATCCA 750
   |||||
QY 913 TGGAT 917
   |||||
Db 751 TGGAT 755
   |||||

```

Search completed: February 13, 2003, 21:06:29  
Job time : 103 secs

Result No.	Query	Score	Match	Length	DB	ID	Description	
1	1484.8	85.0	1488	9	US-09-938-842A-704		Sequence 704, App	
2	744.2	42.6	1473	9	US-09-938-842A-786		Sequence 786, App	
3	712.6	40.8	1635	9	US-09-938-842A-2344		Sequence 2344, App	
4	643.4	36.8	1833	9	US-09-938-842A-2334		Sequence 2334, App	
5	531.8	30.4	2230	10	US-09-828-313-26		Sequence 26, Appli	
6	507.8	29.1	1638	9	US-09-938-842A-1859		Sequence 1859, App	
7	448.2	25.7	455	10	US-09-770-444-571		Sequence 571, Appli	
8	444.6	25.4	1602	9	US-09-938-842A-2304		Sequence 2304, App	
9	277.8	15.9	1387	10	US-09-828-313-13		Sequence 13, Appli	
10	227.4	13.0	955	10	US-09-770-445-326		Sequence 326, Appli	
11	221.6	12.7	2253	10	US-09-828-313-25		Sequence 25, Appli	
12	200.6	11.5	1800	9	US-09-938-842A-1063		Sequence 1063, App	
13	193	11.0	719	9	US-09-938-842A-3678		Sequence 3678, App	
14	189.6	10.9	2374	10	US-09-854-731-3		Sequence 3, Appli	
15	168	9.6	413	10	US-09-878-574-3809		Sequence 3809, App	
16	159.8	9.1	1372	10	US-09-817-181-1		Sequence 1, Appli	
17	155	8.9	267	10	US-09-923-876-331		Sequence 331, App	
18	145.6	8.3	1074	9	US-10-024-036B-3		Sequence 3, Appli	
19	145.6	8.3	1578	10	US-09-835-788A-6		Sequence 6, Appli	

QY 247 AAGCTCGTGTGCGGAGGATTAACAAGATGATGCGCTGAGATTCAGATCATGATCAT 306  
 Db 181 AAGCTCGTGTGCGGAGGATTAACAAGATGATGCGCTGAGATTCAGATCATGATCAT 240  
 QY 307 CTCTCTGAGATCCAAATGTTGTTAGGATCAAGGAGCTTATGAAGATTCGGTCTTTGTT 366  
 Db 241 CTCTCTGAGATCCAAATGTTGTTAGGATCAAGGAGCTTATGAAGATTCGGTCTTTGTT 300  
 QY 367 CATATTGTTATGGAGTTTGTGAAGTGGTGAAGCTTTTGTATGATGATGTTTCTAAAGGT 426  
 Db 301 CATATTGTTATGGAGTTTGTGAAGTGGTGAAGCTTTTGTATGATGATGTTTCTAAAGGT 360  
 QY 427 CATTTTAGTGAAGTGAAGCTGTAAGCTTATTAAGAGATTCCTGTTGTTGTTGAGGCT 486  
 Db 361 CATTTTAGTGAAGTGAAGCTGTAAGCTTATTAAGAGATTCCTGTTGTTGTTGAGGCT 420  
 QY 487 TGTCATCTCTTGGTGTATGATGAGATCTCAAACTCGAGAATTTCTTGTGTTGATGT 546  
 Db 421 TGTCATCTCTTGGTGTATGATGAGATCTCAAACTCGAGAATTTCTTGTGTTGATGT 480  
 QY 547 CTTAAGATGATCTAAGCTTAAGGCTACCGATTTTGGTGTCTCTCTTATTAAGCCA 606  
 Db 481 CCTAAGATGATCTAAGCTTAAGGCTACCGATTTTGGTGTCTCTCTTATTAAGCCA 540  
 QY 607 GGCAATATTTATATGACGTAGTTGGAAGTCCGTACTATGTTGTCACCAAGAGTGTCTAAG 666  
 Db 541 GGCAATATTTATATGACGTAGTTGGAAGTCCGTACTATGTTGTCACCAAGAGTGTCTAAG 600  
 QY 667 AATGTTATGGACTGAATAGATGTTGAGAGTGGTGTGTTTATCTCTACATTTTACTC 726  
 Db 601 AATGTTATGGACTGAATAGATGTTGAGAGTGGTGTGTTTATCTCTACATTTTACTC 660  
 QY 727 AGCGGTCTCTCCCTCTCGGAGAGATGAGTCTGGAATCTTTAGACAGATATTGCAA 786  
 Db 661 AGCGGTCTCTCCCTCTCGGAGAGATGAGTCTGGAATCTTTAGACAGATATTGCAA 720  
 QY 787 GGAAGTTAGATTCAAACTGACCCGTGCTACTATCTCAGAGCTGCTTAAGATTTG 846  
 Db 721 GGAAGTTAGATTCAAACTGACCCGTGCTACTATCTCAGAGCTGCTTAAGATTTG 780  
 QY 847 ATCTATAAATGCTCGAAGAGGAGCCCAAGAAAGCATTTCTGCTCATGAAGCTTTGT 906  
 Db 781 ATCTATAAATGCTCGAAGAGGAGCCCAAGAAAGCATTTCTGCTCATGAAGCTTTGT 840  
 QY 907 CACCCATGATTTGCTGATGAACAGAGAGCCCAAGAAAGCATTTCTGCTCATGAAGCTTTGT 966  
 Db 841 CACCCATGATTTGCTGATGAACAGAGAGCCCAAGAAAGCATTTCTGCTCATGAAGCTTTGT 900  
 QY 967 TCTCGTCTAAGCAATTTCTCAATGAATTAAGAAATGATGATTCGGGTAAAT 1026  
 Db 901 TCTCGTCTAAGCAATTTCTCAATGAATTAAGAAATGATGATTCGGGTAAAT 960  
 QY 1027 GCTGAGAGCTTTTCAGAGGAGAAATTTGAGGTCTGAAGAAATTTTCAGATGATGAC 1086  
 Db 961 GCTGAGAGCTTTTCAGAGGAGAAATTTGAGGTCTGAAGAAATTTTCAGATGATGAC 1020  
 QY 1087 ACAGACACAGCGAAAGATTTTGAAGCTCAAGCGGTTTGAAGAGATTCGGA 1146  
 Db 1021 ACAGACACAGCGAAAGATTTTGAAGCTCAAGCGGTTTGAAGAGATTCGGA 1080  
 QY 1147 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAACT 1206  
 Db 1081 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCGACAACT 1140  
 QY 1207 GGTCAATAGACTACGGAATTTCTAGCAGCAACCTTACATGACAAAGATGGAGAGA 1266  
 Db 1141 GGTCAATAGACTACGGAATTTCTAGCAGCAACCTTACATGACAAAGATGGAGAGA 1200  
 QY 1267 GAGGAGATTTCTGGTGTGCTTTTTCGCACTTTGCAAAAGACGGAAGCGGTTATATCACC 1326  
 Db 1201 GAGGAGATTTCTGGTGTGCTTTTTCGCACTTTTTCGCAAAAGACGGAAGCGGTTATATCACC 1260

QY 1327 ATCGATGAGCTTCAGTTCAGCTTGACAGAGTTTGTCTATGATACACCTCTGGACGAC 1386  
 Db 1261 ATCGATGAGCTTCAGTTCAGCTTGACAGAGTTTGTCTATGATACACCTCTGGACGAC 1320  
 QY 1387 ATGATCAAGGAGATTTGATCTTGACAATGACGGAAGATGATTTCTCGGAGTTTACAGCA 1446  
 Db 1321 ATGATCAAGGAGATTTGATCTTGACAATGACGGAAGATGATTTCTCGGAGTTTACAGCA 1380  
 QY 1447 ATGATGAGGAAGAGATTTGAGTTGGGAGAGCAGACCATGATGAAGAACTTTGAACCTTC 1506  
 Db 1381 ATGATGAGGAAGAGATTTGAGTTGGGAGAGCAGACCATGATGAAGAACTTTGAACCTTC 1440  
 QY 1507 AACATTGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGACTGA 1554  
 Db 1441 AACATTGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGACTGA 1488

RESULT 2

US-09-938-842A-786  
 ; Sequence 786, Application US/09938842A  
 ; Patent No. US20020160378A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harber, Jeff  
 ; APPLICANT: Kzepe, Joel  
 ; APPLICANT: Wang, Xun  
 ; APPLICANT: Zhu, Tong  
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
 ; FILE REFERENCE: SCRIPI300-3  
 ; CURRENT APPLICATION NUMBER: US/09/938,842A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 786  
 ; LENGTH: 1473  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-938-842A-786

Query Match 42.6%; Score 744.2; DB 9; Length 1473;  
 Best Local Similarity 70.0%; Pred. No. 3.4e-158;  
 Matches 1001; Conservative 0; Mismatches 428; Indels 0; Gaps 0;  
 QY 106 GTTCTACCATATCAACACACCCAGATTAAAGAGATCAATTACCTTCTGGGAAAAAGCTAGGC 165  
 Db 28 GTTCTTCTTACAGACCAAAAACGTTGAAGACAATTACTTTCTTGGTCAAGTCCCTTGA 87  
 QY 166 CAAGGCCAATTTGGACACACCTTATCTGACAGAGAAATCAACCTCGCTAAATTACGCC 225  
 Db 88 CAAGGCCAATTTGGACACCACTTTCTCTGTACCCATAAACAGACAGGTCAAAGCTTGC 147  
 QY 226 TGCAAAATCGATCCGAGGCGAAAGCTCGTGTCTCGAGGATTACGAAGATGTATGGCGT 285  
 Db 148 TGCAAAATCCATACCCAAAAGGAGTCCCTTTGTCAAGAAGATTACGACGAGCTTCTGAGA 207  
 QY 286 GAGATTGAGATCATGATCATCTCTGAGCATCCAAATGTTGTAGGATCAAGAGGACT 345  
 Db 208 GAGATCCAGATATGATCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 267  
 QY 346 TATGAAGATTTCGGTGTGTTGTTTCATATTGTTATGGAGGTTTGTGAAGGTTGGTGAAGCTTTT 405  
 Db 268 TACGAGACACCAAAAACGTCGATCTTTGATGGAGCTTTGTGAAGGAGGTGAGTTGTT 327  
 QY 406 GATCGGATTTTCTTAAAGGTCAATTTTACTGAGCGTGAAGCTGTCAAGCTTATTAAAGCG 465  
 Db 328 GATAGAATTCTGAAGAGAGGTCTATTACGTGAAGAGAGAGCTGCTTAAGCTTATCAAGACC 387  
 QY 466 ATTCTTGGTGTGTTGAGGCTTGTCTATTCTTCTTGGTGTGTTATGATGATGATGATGATGATG 525

```

Db 398 ATTGTTGGGTTGTGAGCGTGTCACTCTCTGGTGTGTTTCATAGATCTTTAGCCT 447
Qy 526 GAGAAATTTCTGTTTGTAGTCCCTAAAGATGATGCTTAAGCTTAAGGCTACCGATTTTGGT 585
Db 448 GAGAAATTTCTGTTTGTCTCTGATGAAGATGCTCTCTTAATCTACTGACTTTGGC 507
Qy 586 TTGCTGCTCTTCTATAACCCAGGACAAATTTATATACGCTAGTTGGAAGTCCGTACTAT 645
Db 508 CTCCTGTTTCTGCACACAGGAGAGCAATTTTCGGAATCTGTTGTAAGTCTTACTAT 567
Qy 646 GTTGACACAGAGGTGCTAAAGAAATTTATGGAACCTGAAATAGATGTTGGAGTGTGGT 705
Db 568 GTGGCACTGAGGTTTACATAAGCAATTTATGCTCCTGAATGTCAGCTATGGAGTGTGGA 627
Qy 706 GTTATCCTCTACATTTTACTCAGGCTGTTCTCCTCTCTGGGACAGAGCTGAGTCTGGA 765
Db 628 GTTATCCTCTACATTTTCTTATGTTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 687
Qy 766 ATCTTTAGACGATATTCGAAGGGAAGTTAGATTTCAAACTGTACCCGTCGCTTACTATC 825
Db 688 ATCTTCAGGAGATTTTACAGGAAAGTTGAGTTTGAGATCAATCTTGGCCTAGCAAT 747
Qy 826 TCAGAGCTGTAAAGATTTGATCTATAAATGCTCGAAAGGAGCCCAAGAACCCATT 885
Db 748 TCAGAGGTGCAAGATCTTATAAAGAAATGCTTGAAGCAATCTTAAAGAGAGGCTA 807
Qy 886 TCTGCTCATGAAGCCTTGTGTCACCCATGCTGATGAACAGAGAGCCCAAGCAAG 945
Db 808 ACTGCTCATCAAGTGTGTGTCATCCGTTGATGTTGGATGATAAGTTGCTCCAGATAA 867
Qy 946 CTTCTGTATCCAGAGCTTTATCTGCTTAAGCAGATTTTCTCAATGAATAGATTAAG 1005
Db 868 CTTTGGACTGCGCGTGTGTCGCGCTGAAGAAGTTCTCTGCAATGAACAACTTAAG 927
Qy 1006 AAAATGGCAATACGGGTAAATGCTGAGAGATTTTCAGAGGAAGAAATGGAGTCTGAAG 1065
Db 928 AGATGGCTTTACGAGTATTTGACAGAGATCTATCTGAGGAGAAATCGGTGTCTCAA 987
Qy 1066 GAATTTGCTCAAGATATAGACACAGAACAGCGAAGATTTCTTTGAGAGCTCAAA 1125
Db 988 GAATGTTTCAAAATGATAGACACAGATAAAAGTGGGATATACGTTTGAAGAGTTAAA 1047
Qy 1126 GCGGTGTTGAAGAGAGTGGGATCTGAATGGAATCAGAAATCAAGTCTCTCATGGAT 1185
Db 1048 GATAGTATGAGAGCTTTGGGTGACAGCTTTATGNAATCAGAGATCCAGAACTCTTGG 1107
Qy 1186 GCGGTGATATCGAACACAGTGGTACATAGACTACGAGAAATTCCTAGCAGCAACCTTA 1245
Db 1108 GCGGTGATGTTGATGAGAGTGAACAAATTCATGAGAGATTTCTTAGTCTCAACATC 1167
Qy 1246 CACATGACAGATGGAGAGAGAGATTTCTGGTGTGCTGATTTTGGACTTTGACAAA 1305
Db 1168 CACTTGAAACAGCTGGAGAGAGAGAGATTTAGTAGTGTGATTTCTTTCTTTTGAAG 1227
Qy 1306 GACGAAGCGGTTATATCACCATCGATGAGTTTCAGTCTGAGCTTTGCACAGAGTTTGGTCTA 1365
Db 1228 GATGCAAGTGGTTACATCACATCGAAGAGCTTCAACAGGCAATGGAAGGATTTGGTATA 1287
Qy 1366 TGTGATACACCTCTGACACATATGATCAAGAGATTTGATCTGACATGACGGAAGATC 1425
Db 1288 AACGATTTCAATCTTGATGAATGATCAAGACATTTGATCAAGATAATGATGGAACAA 1347
Qy 1426 GATTTCTCGAGTTTACAGCAATGATGAGAAAGGAGATGGAGTTGGAGAGAGCAAGC 1485
Db 1348 GACTATGGAGAAATTTGTGCAATGATGAGAAAGAAATGGCACTGGAGGAGGATTTGGT 1407
Qy 1486 ATGATGAGAACTTGAACTTCAACATTTGCTGATGCTTTTGGAGTTGATG 1534
Db 1408 CGGAGAACTATGAGGAACCTCTCTCAACTTTGGAACCTACTCTTCTCTGATG 1456

```

RESULT 3

```

US-09-938-842A-2344
; Sequence 2344, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,966
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2344
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2344

```

Query Match 40.8%; Score 712.6; DB 9; Length 1635;  
 Best Local Similarity 68.3%; Pred. No. 4.6e-151;  
 Matches 988; Conservative 0; Mismatches 459; Indels 0; Gaps 0;

```

Qy 73 ACGAAGCCAAACCCCTAGACGCTCTTCAAACACAGATTTCTACCATTCAAAACACCACGATTA 132
Db 184 ATGGGGGTAAAGTTGTTGACAAATCAATCTTACTATGTTCTTGGTCACAGACTCCTAACATT 243
Qy 133 AGAGATCATTTACCTTTCTGGGAAAAAGCTAGGCCAAGGCAATTTGGAAACAACTTATCTC 192
Db 244 CGTGATCTTTACAGCTTGAGTCGTAGTTAGGACAAAGCAATTCGGGACACGATTTTG 303
Qy 193 TGCACAGAGAAATCAACCTCGCTAATTTAGCTGCAATCGATCCGAGCGAAGAGCTC 252
Db 304 TGTACTGATATGTCACAGGTTGACTATGTTGTTAGTCTATATCCAGAGGAAATTTG 363
Qy 253 GTGTGTGCGGAGGATTCAGAGATGTTATGCGGTGAGATTCAGATCATGCTATCTCT 312
Db 364 ATATCTAAAGAAAGATGTTGAGGATGTTAGGAGGAGATTCAGATTATGCAATTTAGCT 423
Qy 313 GAGCATCCAAATGTTGTAGGATCAAGGACATTTAGAGATTCGCTGTTTGTTCATAT 372
Db 424 GGTCAAGAAATATTTGTTACTATTTAAAGGAGCTTATGAGGATCCTTTGTATGTTCAAT 483
Qy 373 GTTATGGAGGTTTCTGAAGGTGGTGGCTTTTTCGCGGATTTTCTTAAAGGTCAATTT 432
Db 484 GTGATGGAGCTTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 543
Qy 433 AGTGAGCTGAAGCTGCAAGCTTATTAAGACGATCTTGGTGTGTTGGTGGTGGTGGTGGT 492
Db 544 AGCGAGAGAAAGCTGCTGAGTTGACCAAGATCATTTGCGTGTGTTGTTGAGGCGTGTCA 603
Qy 493 TCTCTTGGTGTATGTCATAGATCTCAAACCTCGAGAAATTTCTTGTGTTGATAGTCTCTAA 552
Db 604 TCTCTTGGTGTATGTCATAGATTTAAAGCTCGAGAAATTTCTTGTGTTGTTGTTGTTG 663
Qy 553 GATGATGTAAGCTTAAGGCTACCGATTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTG 612
Db 664 GATGATTTCTCTCTTAAGGCCATTTGATTTTGGTCTCTCTCTCTCTCTCTCTCTCTCT 723
Qy 613 TATTTATATGAGCTAGTTGGAAGTCCGCTACTATGTTGCCACAGAGGTGCTTAAAGAAATGT 672
Db 724 ATATTCAGAGGATGTTGTTGGAAGTCCATCTATGTTGCTCTCTGAGGTTCTTCTTAAACAT 783
Qy 673 TATGACCTGAAATAGATGTTGGAGTCTGGTGTGTTATCTCTTACATTTTACTCAGCGGT 732
Db 784 TATGTCAGAGAGCTGATGTTGGACTGCTGGTGTGTTATCTCTATATCTTACTTAAAGTGT 843

```

733 GTCTCCCTTCTGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTCGAAGGAG 732  
Db 844 GTCCCGCTTCTGGCAGAAACACAGAGGAATATTGTGTTGAAGGGATAT 903  
Qy 793 TTAGATTTCAAAATCTGACCCGCTGCTACTCTCAGAAAGTGTCTAAAGATTGATCTAT 852  
Db 904 ATTGACTTTGATACAGACCCGCTGGCTGTCTATATCCGACAGTCTAAAGATCTGATCCG 963  
Qy 853 AAAATGCTGAAAGAGCCCAAGAAAGCAATTTCTGCTCATGAGCCTTGTGTCACCA 912  
Db 964 AAGATGTTATGCTAGTCTCTGAAAGTTTGAAGTCTCATGAGTCTTCCGTCATCCA 1023  
Qy 913 TGATGTTGATGAAACAGACAGACAGCAAGCCTCTTGTATCCAGAGTCTTATCTCGT 972  
Db 1024 TGATCTGTGAGATGAGATGTCACCGGATAGACACTTGACCCGGCTGTTTGTCTCGT 1083  
Qy 973 CTAAAGAGTTTCTCAATGATTAAGATTAAGAAATGGAATTAAGGTTAATGCTGAG 1032  
Db 1084 CTAAAGAGTTTCTCAATGATTAAGATTAAGAAATGGAATTAAGGTTAATGCTGAG 1143  
Qy 1033 AGACTTTGAGAGGAAGAAATGAGGTCTGAAGGAATTTTCAAGATCATAGACAGAC 1092  
Db 1144 AGCTCTCAGAGAGAGATGCGGTTTAAAGCAATGTTGAGCAATGATGAT 1203  
Qy 1093 AACAGCGAAAGATTAATCTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTGGATCTGAA 1152  
Db 1204 AACAGCGGTGCAATCACTTTGATGAATCAAGAGCTGAGGCTTGAAGAGATATGGATCAAC 1263  
Qy 1153 CTGATGGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAAAGTGTACA 1212  
Db 1264 TTGAAGACACCGAGATCCAGATCTTATGGAAGCGGCTGATGTGACAAACAGCGGTACA 1323  
Qy 1213 ATAGACTACGAGAAATTCCTAGCAGCAACTTACATGAAACAGATGAGAGAGAGAG 1272  
Db 1324 ATAGATACAGAGATTTATGAGCGAGATCCATCTGAATTAATCTAGAGAGAGAGAG 1383  
Qy 1273 ATTCTGGTGGCTCAATTCGGACTTTGCAAGAGCGGAGGTTTATATCACCATCGAT 1332  
Db 1384 CATCTGCTCTGCAATTCAGTACTTTGCAAGAGTGAAGTGGTTTATCATCACCATTGAT 1443  
Qy 1333 GAGCTTCAGTCACTTGCACAGAGTTTGTCTATGTGATACACCTCTGAGCAATGATC 1392  
Db 1444 GAGCTGCAACAATCTTGATTAAGATGAGATGAGATGAGATGAGTCTTCTTGAAGACATAATC 1503  
Qy 1393 AAGGAGATGATCTGACATGACGGAGATCGATTTCTCGAGTTTACAGCAATGATG 1452  
Db 1504 AAGAAGTAGATCAAGACACGATGACGGATTGATTAAGAAATTTGTCGAGATG 1563  
Qy 1453 AGAAAGGAGATGAGTTGGGAGAGCAGACCAATGATGAAGAACTTGAATTTCAACATT 1512  
Db 1564 CAAAGGGAAATGCTGGTGTAGGAGAGAGAAACAATGAAAAATAGTCTAAACATCAGCATG 1623  
Qy 1513 GCTGATG 1519  
Db 1624 AGAGATG 1630

RESULT 4  
US-09-938-842A-2334  
; Sequence 2334, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Krepes, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2334  
; LENGTH: 1833  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2334

Query Match 36.8%; Score 643.4; DB 9; Length 1833;  
Best Local Similarity 54.7%; Pred. NO. 1.8e-135;  
Matches 956; Conservative 0; Mismatches 521; Indels 0; Gaps 0;

Qy 39 TCGAAGAAGAACCAACAAACCAAAATGGAGACGAAGCCAAACCTTAGACGTCTTC 98  
Db 345 TCGAGTAAACCTTAAGAGCCTAAACACATGAAGAGAGTGTCAAGTGCAGGCTTAGGAC 404  
Qy 99 AAACACAGTTCTACATATCAACACACAGATTAAGAGATCATTCTCTGGGAAAAA 158  
Db 405 TGAGTCAGTGTTCAGAGAGAGACTGAAACCTTCAAGGAATTTCTATCTCTGGGAGGAA 464  
Qy 159 GCTAGGCCAAGCCAAATTTGGAACAACCTATCTCTGACAGAGAAATCAACCTCCGCTAA 218  
Db 465 ACTCGACAGAGGCAATTTGGACGACTTTTATGTGTCGAGAGACTACGGGGAAGGA 524  
Qy 219 TTACGCTTCAAATCGATCCGAAAGCAAGCTCGTGTGTCGCGAGGATTAACGAATGT 278  
Db 525 GTTTCCTGCAAGTGTGCTTAAGAGAGAGCTATTGACTGATGAGGACGTTGAGGATGT 584  
Qy 279 ATGGCGTGAGATTCAGATCATCATCTCTGAGCATCCAAATGTTGTAGGATCAA 338  
Db 585 GAGAAGAGAAATTCAGATTAATGATCATCTGCGCTGTCACCTTATGTCTCATCTCCATCA 644  
Qy 339 AGGAGCTTATGAAGATTCGCTGTTTGTTCATATTGTTATGAGAGTTTGAAGGTGTGA 398  
Db 645 AGGAGCTTATGAGGATGTTGTGGCAGTGCACCTTGTAAATGAGTGTGTGCGAGCGCGA 704  
Qy 399 GCTTTTGTGATCGATGTTCTAAAGGTCAATTTAGTACGCGTGAAGCTGCAAGCTTAT 458  
Db 705 GCTTTTGTACAGATCATTAACCGGCTCACTACAGAGAGGAAAGCGCTGAGCTCAC 764  
Qy 459 TAAGACGATTTCTGCTGTTTGTGAGGCTTGTCTCTTGTGTTATGATAGAGATCT 518  
Db 765 TAGAACCATTTGTTGGGTTGTAGAGGCTTGCCATTTCTTGGTGTATGATCGAGACCT 824  
Qy 519 CAAACCTGAGATTTCTGTTTGTAGGCTTGTCTCTTGTGTTATGATAGAGATCT 578  
Db 825 CAAAGCCGAGATTTCTGTTTGTGAGTAAACAGAGATTCCTCTTGTGAGAGCGATTGA 884  
Qy 579 TTTTGGTTTGTCTGCTCTTCTATAAGCCAGGACAATATTTATATGACGTAGTTGGAATCC 638  
Db 885 TTTTGGACTCTCCATGTTCTTTAAACACAGACGATGTTTTTACAGATGTTGTTGTTAGCC 944  
Qy 639 GTACTATGTTGACAGAGGCTCTAAAGAAATGTTATGACCTGAATAGATGTTGCGAG 698  
Db 945 ATATTATGTTGCCCCAGAGTTCTTTCGAAAGCGTTATGCCCCCTGAAGCTGATGTTCTGAG 1004  
Qy 699 TGCTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCTCCCTTCTGGGCGAGACTGA 758  
Db 1005 TGCTGAGTATGTTGTACATTTTATTAAGCGGAGTTCTCTCAATCTGGGCTGAAACCGA 1064  
Qy 759 GTCGGAATCTTTAGACAGATTTGCAAGGGAGTGTAGATTTCAAACTGACCGTGGCC 818  
Db 1065 ACAAGGTATTTTGAACAGGTCCTCCAGGTGATCTTGACTTTTGTGCTCCGATCCATGGCC 1124  
Qy 819 TACTATCTCAGAGGCTCTAAAGATTTGATCTATAAATGCTCGAAAGGAGGCCCAAGAA 878  
Db 1125 AAGTATATCTGAAGTGAAGAGATTTAGTAGGAAATGCTTGTGCGAGGATCCCAAGAA 1184  
Qy 879 ACGCAATTTCTCATGAAGACCTTTGTGTCACCCATGGATTTGTCGATGAACAGACGACC 938



```

Db 1682 CAACGAGTTTCATATCGGCAACAATGCACATGAACAGACGAGAAAGAGATCACCTTTG 1741
Qy 1281 GCTGCTATTTTCGGGACTTTGACAAAGACGGAAGCGGTTATATACCATCGATGAGTTTCA 1340
Db 1742 GGCAGCATTCATGCTATTCGACGCGACAATAGCGGGTATATCACCATCGACGAGTTCA 1801
Qy 1341 GTCAGCTTGCACAGAGTTTGGTCTTATGTATAC---ACCTTGGACGACATGATCAAGGA 1397
Db 1802 GGAAGCAATGGAGAAATGGAATGGAGATCCTGAGACCATCCAAAGAGATCATCAGCGA 1861
Qy 1398 GATTGATCTTGACATGACGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAGAA 1457
Db 1862 GGTGACACAGACAACGACGAGAGATGATGACAGAGTTCTGATGCCATGATGCCAA 1921
Qy 1458 AGAGATGAGTTGGGAGAGACGAGCAACCATGATGAAGAA 1496
Db 1922 GGGCAATCCTGCGCTGAAACCGGAGGAACGTTGAACAA 1960

RESULT 6
US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Query Match 29.1%; Score 507.8; DB 9; Length 1638;
Best Local Similarity 61.7%; Pred. No. 5.6e-105;
Matches 828; Conservative 0; Mismatches 507; Indels 6; Gaps 1;

Qy 131 TAAGAGATCATACCTTCTCGGGAAGAAAGCTAGGCCAAGGCCAATTTGGAACAACCTATC 190
Db 176 TCAGCGCAAAATACATCTTAGTTCGTGAATTAGTTCGAGCGGAATTCGGAATCACTTACC 235
Qy 191 TCTGCACAGAGAATCAACCTCGCTAAATACGCTGCAAAATCGATCCGGAAGCGAAAGC 250
Db 236 TCTGTACTGATCGTGAACCCAGAGCTTTAGCTTGCAAAATCGATTCAAAGCGAAAGC 295
Qy 251 TCGTGTCTCGGAGGATTACGAAGATGTATGCGGTGAGATTCAGATCATCATCTCTCT 310
Db 296 TTCGAACAGCTGTGATATCGAAGAGCTTCGTCGTGAGGTAGCGATTATGTCTACTTTAC 355
Qy 311 CTGAGCATCAAAATGTTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGTTTCATA 370
Db 356 CTGAGCATCAAAAGCTAGTTAAGCTTAGCTAGTTATGAGGATACGAGAACGTTGCTATC 415
Qy 371 TTGTTATGAGGTTTGTGAAGGCTGTTGAGCTTTTTCATCGGATTTGTTCTAAAGGTCATT 430
Db 416 TGGTTATGAGCTTTGTGAAGGAGGTGAGCTTTTTCATCGGATTTGTTCTAGAGACATT 475
Qy 431 TTAGTACGCTGAGCTGTCAAGCTTATTAAGACGATTCTTGGTGTGTTGAGGCTTCTC 490

```

```

Db 476 ACACGAGCGTGTCTGCTGAGCTGTTGCGAGAACGATTGCTGAGGTTGTGATGATGTC 535
Qy 491 ATTCTCTTGTGTTATGATAGATGCTCAAACCTGAGAAATTTCTTGTGATGATGCTTA 550
Db 536 ACTCTAATGGAGTTATGATCGAGATTGAAACCTGAGAAATTTCTTGTGTAATAAAA 595
Qy 551 AAGATGATGCTTAAGCTTAAGGCTACCGATTGTTGTTGTTGCTGCTTCTATTAAGCCAGGAC 610
Db 596 AGGAAATTTCTCCACTAAAGCTATTGATTTTGGCTTGTGTTCTTCAACACCTGGAG 655
Qy 611 AATATTTATGACGTAGTTGGAAGTCCGTACTATGTTGCACAGAGGTGCTAAAGAAAT 670
Db 656 ATAAGTTTACAGAGATTGTAGGAAGTCCGTATTATATATGCTCCAGAAAGTGTGAAGAG 715
Qy 671 GTTATGACCTGAAATAGATGTGAGAGTCTGCTGTATCCCTCTACATTTTACTCAGCG 730
Db 716 ATTATGGACAGGGGTTGATGTGAGAGTCCGAGTTATATCTATATCTTCTGCTCTG 775
Qy 731 GTGTTCTCTCTCTGCGGACAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGA 790
Db 776 GTGTTCTCTCTCTGCGGCTCAGACTGAACAAGTGTGCTCTTGGCATCTTGGCGGAG 835
Qy 791 AGTTAGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAAAGCTGCTAAAGATTTCATCT 850
Db 836 TTCTTGATTTTAAAGAGAGACCCCTTGGCTCAGATATCAGAGATGCGAAGAGCCTTGTGA 895
Qy 851 ATAAATGCTCGAAAGGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCCTTGTGTACC 910
Db 896 AGCAGATGTTGATCCCTGATCCGACTAAGCGGTTAACTGCTCAGCAAGTGTAGCTCACC 955
Qy 911 CATGATTTGCTGATGAACAGACGACACACAAAGCTCTTGTATCCAGAGCTTTATCTC 970
Db 956 CATGATACAGAAATGCAAAAGAAAGCTCCCAATGTTCTTTAGGAGATATAGTCAGATCTA 1015
Qy 971 GTCTAAAGCAGTTTCTCAATGAATGAATTAAGAAATGGAATTTACGGGTAAATGCTG 1030
Db 1016 GGTTCAGAGCTTCTCTATGATGAACAGATTCAAAAGAGAGTCTTCGTGTAATTGCGG 1075
Qy 1031 AGAGACTTTCAGAGGAAGAAATTCGAGTCTGAAGGAAATTTTCAAGATGATAGACACAG 1090
Db 1076 AGCACTTGTCTATTCAAGAGGTTGAAGTGATAAAGAACATGTTCTCTACTGATGATG 1135
Qy 1091 ACAACAGCGGAACGATTACTTTTGAAGAGCTCAAAAGCGGTTTGAAGAGAGTCGGATCTG 1150
Db 1136 ACAGGATGTTAAATTAATCTTACCAGGAACTCAAGGCTGGGCTCAGAAAGTGGTTTAC 1195
Qy 1151 AACTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGTGATATCGACAACAGTGGA 1210
Db 1196 AACTTGGTGAACAGAGATCAAAATGTTGATGGAAGTGGCGGATGTCGATGGAAATGGGT 1255
Qy 1211 CAATAGACTACGGGAATTCCTTAGCAGCAACCTTACACATGAAACAAGATGGAGAGAGG 1270
Db 1256 TTCTGATTTATGAGAGGTTTGTAGCTGTGATTAATCTACTTGCAGAAATAGAGAAATG 1315
Qy 1271 AGATTCTGTGCTGCTCAATTTTGGGACTTTTGAAGAGCGGAGCGGTTATATCACCATCG 1330
Db 1316 AACTTTTCAAACTAGCTTTTATGTTTTCGACAAAGATGGAAGTACATACATTTGAACCTG 1375
Qy 1331 ATGAGCTTCAGTCAGCTTGCACAG-----GTTTGTCTATGTGATACACCTCTGGACG 1384
Db 1376 ATGAGCTACGGGAAGCTTTAGCGGATGAGTTAGCGGAGCCAGACCCAGCTGTTCTAGCG 1435
Qy 1385 ACATGATCAAGGAGATTGATCTTGACAAATGACGGGAAGATCGATTTCTCGAGGTTTACAG 1444
Db 1436 ACATCATGCTGAAGTTGACACTGACAAAGGACGAGCGTATAAACTATGATGAGTTTGTGA 1495
Qy 1445 CAATGATGAGGAAGAGATG 1465
Db 1496 CGATGATGAAGCTGGAACGTG 1516

```

RESULT 7  
US-09-770-444-571

Query Match	25.4%	Score 444.6	DB 9	Length 1602
Best Local Similarity	59.7%	Prod. No. 9.4e-91		
Matches 788	Conservative 0	Mismatches 524	Indels 9	Gaps 2
Qy	142	TACCTTCTCGGAAAAAAGCTAGGCCAAGGCCAAATTGGAAACAACCTATCTCTGCACAGAG	201	
Db	169	TATGATCTCGGGCGTGAGGTTGGTCGCGAGAGTTTGGTATTACTTACTTGTGCATGAT	228	
Qy	202	AAATCAACCTCCGCTAAATTAGCCTGCAAAATCGATCCGAAGCGAAAGCTGCTGTCTCC	261	
Db	229	ATCAAAACGGCGAAGAAGTATGCGTGCAGGCTATATCAAAAGAAGAAGCTTAGACAGCT	288	
Qy	262	GAGGATTACGAGATGTATGGCTGAGATTCAGATCATGATCATCTCTCTGAGCATCA	321	
Db	289	GTGGATATAGAGATGTTTAGGAGGAAGTTGAGATAATGAATGAACATATGCTACACACCA	348	
Qy	322	AATGTTGTTAGGATCAAAAGGGACTTATCAAGATTCCGGTGTGTTGTTTCATATGTTATGGAG	381	
Db	349	AAATCGTGTCTGAGGATGCCCTTTGAGGATGATGATGCAGTGCATATAGTTATGGAG	408	
Qy	382	GTTTGTGAAGGTGGTGAAGCTTTTTCGATCGGATGTTGTTCTTAAAGTCATTTTAGTGAGCGT	441	
Db	409	TTGTGTGAAGGAGGTGAGCTGTTTTCGATCGGATGTTGCTAGAGTCATTATACTGAGCGCA	468	
Qy	442	GAAGCTGTCAAGCTTTATTAAGACGATCTTCGGTCTGTTGAGGCGTGTCTATTCTCTTGT	501	
Db	469	GCTGCTGCTGCACTGATGAAGACTATTCTTGAAGTTGTTAGATATGCCATAAGCATGGA	528	
Qy	502	GTTATGCATAGAGATCTCAAAAGCTGAGAAATTTCTTGTTCATAGTCTTAAAGATGATGCT	561	
Db	529	GTGATGCATCGGAATCTAAGCCTGAGAACTTCTCTTTGCCAAATAAAGAGAGACATCA	588	
Qy	562	AAGCTTAAAGCTACCGATTTTGGTTTGTCTGTCTCTCTATTAAGCCAGACAAATTTATAT	621	
Db	589	GCCTTTAAAGCCATAGATTTTGGATTTACGTCTCTTCTCAAGCGCTGTGAGGATTTCAAC	648	
Qy	622	GAGGTAGTTGGAGTCCGTACTATGTTCCACACAGGTGCTTAAGAAATGTTATGGACCT	681	
Db	649	GAGATGTTTGAAGTCCCTTATTACATGCGCACAGAGTACTTAGGGCGAAATTAAGGACCT	708	
Qy	682	GAATATAGATGTGTGGAGTGCTGGTGTATCTCTACATTTTACTTCAGCGGTGTTCTCC	741	

Db 709 GAGGTGATCTGGAGTCTGAGTATCTCTTATATCTCTGCTCTGTGTGCCACCA 768  
Qy 742 TTCTGGGAGAGTCTGAGTCTGGAATCTTTAGACAGATATTCGACGGAAGTTAGATTTC 801  
Db 769 TTTTGGCCGAGACTGAGCAAGGGTGGCTCAGCGATCATAGTGTGATGATGATTTT 828  
Qy 802 AAATCTGACCCGTGGCTACTATCTCAGAAAGTCTGCTAAAGATTTGATCTATAAAATGCTC 861  
Db 829 AAGAGGATCCATGCGCGAGAGTTCTGAGACTGCGCAAGACCTTGTGAGGAAGTCTC 888  
Qy 862 GAAAGAGGCCCAAGAAAGCGATTTCTGCTATGAGCGCTTGTGTCACCAATGATGTC 921  
Db 889 GAACCTGAGCCCAAAAGCGCTTTCTGCTGACAAAGTACTCGAACATTTCTTGGATCAA 948  
Qy 922 GATGAACAGCAGCAGCAGCAAGCTCTTGTATCCAGAGTCTTATCTCGTCTAAAGCAG 981  
Db 949 AATGCGAAGAGCTCCAAATGTTTCACTCGCGAGAGCGGTGAGACGAAAGTCTCAACAG 1008  
Qy 982 TTTTCTCAATGAATGAATTAAGAAATGGAATTAAGGATTAAGGATTTGCTGAGAGACTTTCA 1041  
Db 1009 TTTTCTGTTATGAACAAGCTCAAGAAAGAGCGGTACCGGTGATAGCCGAAACACTTATCA 1068  
Qy 1042 GAGGAGAAATTCGAGTCTGAGGAAATTTTCAAGATGATAGACACAGCAACAGCGGA 1101  
Db 1069 GTGGAGGAGTACTGGCATCAAGGAGCATTTGAGATGATGACAGTAAAGACGCGGA 1128  
Qy 1102 ACGATTACTTTGAAGAGTCAAGCGGTTTGAAGAGTCCGATCTGAACTGAT---G 1158  
Db 1129 AAGATAAACCTCGAGGAGCTTAAATTTGGACTTCATAAACTCGGACAGCAGATACCT 1188  
Qy 1159 GAATCAGAAATCAAGTCTCTATGATGCGGTGATATCGACACAGTGGTACATGAC 1218  
Db 1189 GATACTGATCTACAGATCTGATGGAAGTCTGATGTTGATGGGATGGGACTTTAAAT 1248  
Qy 1219 TAGCGAGAAATCTTAGCAGCAACCTTACACATGAACAAGATCGAGAGAGAGATTTCTG 1278  
Db 1249 TATGGGAGTTTGTGGCTGCTCTGTGCTCTTAAGAAATGGCAACGACGACACTG 1308  
Qy 1279 GTGGCTCATTTTGGGCTTTGACAAAGACGAGGAGGTTATATCACCATCATAGCTT 1338  
Db 1309 CATAAAGCTTTTGGCTTTTGGACCAAGATCAGAGCGATTTACATAGAGATTGAGGAGCTG 1368  
Qy 1339 CAGTCAGCTTGCACAGA-----GTTTGGTCTATGTGATACACCTCTGACGACATGATC 1392  
Db 1369 CGTGAAGCTTTAATGATGAGTGGATTAACAGTGAAGAGTCTTGCACCTATTATG 1428  
Qy 1393 AAGAGATTGATCTTGAATGACGAGGAGATCGATTTCTCGGAGTTTACAGCAATGATG 1452  
Db 1429 CAAGATCTTGACACAGCAAGGACGCGAATAAGCTATGAAGAGTTTGGCGCGATGATG 1489  
Qy 1453 A 1453  
Db 1489 A 1489

RESULT 9  
US-09-828-313-13  
; Sequence 13, Application US/09828313  
; Patent No. US20020059662A1  
; GENERAL INFORMATION:  
; APPLICANT: COSTA e SILVA, OSWALDO DA  
; APPLICANT: BOHNERT, HANS J.  
; APPLICANT: THIELEN, NOCHA VAN  
; APPLICANT: CHEN, ROUYING  
; APPLICANT: SARRIA-MILLAN, RODRIGO  
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
; TITLE OF INVENTION: USE IN PLANTS  
; FILE REFERENCE: 16313-0032  
; CURRENT APPLICATION NUMBER: US/09/828,313  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/196,001  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.1.1  
; SEQ ID NO 13  
; LENGTH: 1387  
; TYPE: DNA  
; ORGANISM: Physcomitrella patens  
; FEATURES:  
; NAME/KEY: modified\_base  
; LOCATION: (1385)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-09-828-313-13  
  
Query Match 15.98; Score 277.8; DB 10; Length 1387;  
Best Local Similarity 63.45; Pred. No. 3.1e-53; Indels 2; Gaps 2;  
Matches 457; Conservative 0; Mismatches 262;  
  
Qy 141 TTACCTCTTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAAACACCTATCTCTGCACAGA 200  
Db 650 TTACATCTTGGGACGGGAGCTTGGCGAGGCGAGTTCGGAGTGACTTACTTGTGTACTGA 709  
Qy 201 GAAATCAACCTCCGCTAATTAGCGCTGCMAATCGATCCGAGGGAAGCTCGTGTCTCG 260  
Db 710 CAAGATGACGAATGAGCGGTACGGGTGCAAGAGCATCGCAAAACGGAAACTGACCAAGTAA 769  
Qy 261 CGAGGATTACGAAGATGTATGCGGTGAGATTTCAGATCATCATCTCTCTGAGCATCC 320  
Db 770 GAGGATATCGAGGATGTAAAGCGGAGGTTTCAGATTATGATCATCACCTGTCCGGGACACC 829  
Qy 321 AAATGTTGTTAGGATCAAGGAGCTTTTGTATCGGATTTTCTAAAGGTCAATTTAGTGAGCG 440  
Db 890 GCTCTGTCAGGTGCGGAGCTTTCGATCGCATCATTTGCCAAGGGGCATTACAGTGAGCG 949  
Qy 441 TGAAGCTGTCAGAGCTTTAATAAGACGATTTCTGTGTGTGTGTGAGGCTTGTCTATTCTTTGG 500  
Db 950 CGCGGTGCGGATATGTGCAGAGTCACTGTCATGTCGTGTCACAGATGCCACTCATTTAGG 1009  
Qy 501 TGTATGCTAGAGATCTCAACCTGAGAAATTTCTGTTTGTATAGTCTTAAAGATGATGC 560  
Db 1010 GGTCTTCCATCGGATCTCAAGCCAGAGAAATTTCTGTGTGCCAGCAAGGCTGAGGATGC 1069  
Qy 561 TAAGCTTAAGGCTACCGATTTTGGTTTGTCTGTCTTCTATTAAGCCAGACAAATTTATA 620  
Db 1070 GCCTCTGAAGGCCACAGACTTCGGTCTGTCAACTTTCTTTAAGCCAGGAGATGTGTCCA 1129  
Qy 621 TGAGGTAGTTGAAGTCCGATCTATGTTGCCAGAGGTGCTAAGAAATCTTATGAGCC 680  
Db 1130 GGATATTGTTGAAGTGGCTATTACGTGGCCCCCTGAAGTTTGAAGAGAAATTTATGTTCC 1189  
Qy 681 TGAATAGATGTGTGAGTGTGTTTGTCTTCTCTACATTTTACTCAGCGGTGTCTCTCC 740  
Db 1190 TGAGCT-GATGTTTGAGTGCAGGCGTGATTGTGTACATTTCTGTGTGTGTGTACCCCC 1248  
Qy 741 CTTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTCGACGGAAGTTAGATT 800  
Db 1249 CTTCTGGGCTGAACCTGAGCAGGCTATCTTTGACGCTGTCTCAAGGGGCACATAGACTT 1308  
Qy 801 C-AAATCTGACCCGTGGCTACTATCTCAGAAAGCTGCTAAAGATTTGATCTATAAAATGC 859  
Db 1309 CGAGACGAGTCCATGCGCGGAAATCTCCACGGGCTTAAGGATTTGGTGAGGAAATGC 1368  
Qy 860 T 860  
Db 1369 T 1369  
  
RESULT 10  
US-09-770-445-326/c  
; Sequence 326, Application US/09770445  
; Patent No. US20020023281A1

GENERAL INFORMATION:  
 APPLICANT: Gorlach, Jorn  
 APPLICANT: An, Yong-Qiang  
 APPLICANT: Hamilton, Carol M.  
 APPLICANT: Price, Jennifer L.  
 APPLICANT: Raines, Tracy M.  
 APPLICANT: Yu, Yang  
 APPLICANT: Rameaka, Joshua G.  
 APPLICANT: Page, Amy  
 APPLICANT: Matthew, Abraham V.  
 APPLICANT: Ledford, Brooke L.  
 APPLICANT: Woessner, Jeffrey P.  
 APPLICANT: Haas, William David  
 APPLICANT: Garcia, Carlos A.  
 APPLICANT: Kriker, Maja  
 APPLICANT: Slader, Red  
 APPLICANT: Davis, Keith R.  
 APPLICANT: Allen, Keith  
 APPLICANT: Hoffman, Neil  
 APPLICANT: Hurlan, Patrick  
 TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
 TITLE OF INVENTION: thaliana  
 FILE REFERENCE: 2023US (PARA-012PRV)  
 CURRENT APPLICATION NUMBER: US/09/770,445  
 PRIOR FILING DATE: 2001-01-26  
 PRIOR APPLICATION NUMBER: US 60/178,472  
 PRIOR FILING DATE: 2000-01-27  
 NUMBER OF SEQ ID NOS: 999  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 326  
 LENGTH: 955  
 TYPE: DNA  
 ORGANISM: Arabidopsis thaliana  
 US-09-770-445-326

Query Match 13.0%; Score 227.4; DB 10; Length 955;  
 Best Local Similarity 61.4%; Pred. No. 5.8e-42;  
 Matches 401; Conservative 0; Mismatches 246; Indels 6; Gaps 2;  
 QY 811 CGGTGGCTTACTATCTCAGAGCTGCTAAAGATTGATCTATAAAATGCTGAAAGGAGC 870  
 DB 955 CCATGGCTTCTATCTGAAAGCGGAAAGATCTTTAGGAAGATGCTAAACCAAGAC 896  
 QY 871 CCCAAGAAAGCATTTCTGCTCATGAGCCTTGTCACCCATGATGGATGCGATGAACAA 930  
 DB 895 CCGAAGAGACGAATCACGGCTGCACAGGTTCTTGAAATCCTTGA---TCAAAGGGGA 839  
 QY 931 GCAGCACCAGACAAGCCTCTTGATCCAGCAGTCTTATCTCGTCTAAAGCAGTTTCTCAA 990  
 DB 838 GAAGCACCAGACAGCCTTATGATAGCGCTGTGTTATCCGCATGAGCAATCCGAGCA 779  
 QY 991 ATGAATAAGTTAAGAAATGCGATTACGGTAAATGCTGAGAGACTTTCAGAGAGAA 1050  
 DB 778 ATGAACAAGCTTAAAGAGTAGCTCTAAAGTTATTCGGGAGAGTCTATCAGAGAGAG 719  
 QY 1051 ATTGGAGTCTGAGGAATTTTCAAGATGATAGACACAGACAGCGGAGCAATGACT 1110  
 DB 718 ATTAAAGTCTTAAACCAAGTTTGGAAATATAGATACCGAACAAGCGGAGCAATCACT 659  
 QY 1111 TTGAAAGACTCAAAGCGGTTTGAAGAGAGTCGGATCTGAATGAAATCAGAAATC 1170  
 DB 658 TATGAAGAATCAAACCTGGCTAACTAGACTTGGTCTAGACTCTCGGAAACTGAAGTT 599  
 QY 1171 AGCTCTCTGATCGGCTGATATCCACACAGTGTACATAGACTACGGAATTC 1230  
 DB 598 AACCAATCATGGAAGCCGCTACGTCGATGTGTAATGAACAATCGACTACTACGAGTTT 539  
 QY 1231 CTAGCAGCAACTTACACATGAACAGATGAGAGAGAGAGGAGTCTGGTGGCTGCATTT 1290  
 DB 538 ATCTCTGCGACAAATGATAGATACAAATTTAGATCGAGATGAGCATGTATACAAAGCATC 479  
 QY 1291 TCGACTTTGACAAAGCGGAGCGTTTATATCACCATGATGAGCTTCACTGAGCTTGC 1350

DB 478 CAACACTTTGATAAAGACAACACGGCGGCACATACTAGAGATGAGTTGAAAGTGCCATG 419  
 QY 1351 ACAGAGTTTGGTCTATGTGTATGATCACCT---CTGAGCAGCATGATCAAGGAGATTGATCTT 1407  
 DB 418 AAGGATATGGAATGGGAGATGAAGCTAGCATCAAGAAAGTTATATCCGAAGTTGATACC 359  
 QY 1408 GACAATCAGCGGAAGATCGATTCTCGGAGTTTACAGCAATGATGAGGAAAG 1460  
 DB 358 GACAATGATGAAGATAAACTTTGAAGAAATTTTGCCTGATGATGAGAAGTGG 306

RESULT 11  
 US-09-828-313-25  
 ; Sequence 25, Application US/09828313  
 ; Patent No. US20020059662A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COSTA e SILVA, OSWALDO DA  
 ; APPLICANT: BOHNERT, HANS J.  
 ; APPLICANT: THIELEN, NOCHA VAN  
 ; APPLICANT: CHEN, ROUYING  
 ; APPLICANT: SARRIA-MILLAN, RODRIGO  
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
 ; TITLE OF INVENTION: USE IN PLANTS  
 ; FILE REFERENCE: 16313-0032  
 ; CURRENT APPLICATION NUMBER: US/09/828,313  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/196,001  
 ; PRIOR FILING DATE: 2000-04-07  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 2253  
 ; TYPE: DNA  
 ; ORGANISM: Physcomitrella patens  
 US-09-828-313-25

Query Match 12.7%; Score 221.6; DB 10; Length 2253;  
 Best Local Similarity 54.0%; Pred. No. 1.7e-40;  
 Matches 502; Conservative 0; Mismatches 419; Indels 9; Gaps 2;  
 QY 235 ATCCCGAAGCGAAGCTCGTGTGTCGGGAGGATTACGAAGATGATGGCTGTGAGATTTCAG 294  
 DB 564 ATCTCGAAGGAAGATGACGACTGCTATTGCGATCGAGACGCTGGGACGAGAAGTGAA 623  
 QY 295 ATCATGATCATCTCTGAGCATCAAAATGTTGTAGGATCAAGGAGCTTATGAAGAT 354  
 DB 624 ATTTTGAAGGCTCTGCGGAGACACAGAAATTTGGTTGATTTCTACGATTCCTCGAGGAC 693  
 QY 355 TCGGTGTTTGTTCATATTGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTGATCGAAT 414  
 DB 684 CATCTAAATGTGATCTGTTATGGAATTTATGAGGAGTGAATTTTGGATCGAAT 743  
 QY 415 GTTCTAAAGGTCAATTTTAGTGAAGCTGTAAGCTTCAAGCTTATT---AAGACGATCTT 471  
 DB 744 TTGCTCTGGGAGGAAGTACTCGGAGGAAGACCCAAAGGTTGTTGTGCGGAGATTTTG 803  
 QY 472 GGTGTGTTGAGGCTTGTCAATCTCTTGTGTTATGATAGATCTCAAAACCTGGAAT 531  
 DB 804 ACGGTGTGCGTTTGTGTCACCTCAAGGCGTTGTTCCCGAGATCTTAAGCCTGAGAT 863  
 QY 532 TTCTGTTTGTAGTCTCTTAAAGATGATGCTAAGCTTAAGCTACCGATTTTGTGTTGCT 591  
 DB 864 TTCTGTTTACCAGGAAGATGAATATGTCAGCTTAAGCCATTGATTTTGGATTGTCA 923  
 QY 592 GTCTCTATAGCCAGGACATATTTATGACGTAGTTGGAAGTCCGTACTATGTTGCA 651  
 DB 924 GATTTTCATCAACCCGATGAAGACTGAAGATATCTTTGGAAGCCGATACCTACGTTGCG 983  
 QY 652 CCAGAGGTGCTTAAAGAAATGTTATGACCTCAATAGATGTTGGAGTGTGTTGTTATC 711  
 DB 984 CCGGAGGTATTGTCATAGGTTATTTCAATGAAGCTGACGTATGGAGCATTTGGAGTCATC 1043  
 QY 712 CTCTACATTTTACTCAGCGGTGTTCTCCCTTCTGGGACAGAGACTGAGTCTGAAATCTTT 771

```

Db 1044 ACCTACATTTTCTATGTTAGTGCACCGTTTGGGCGCGGACCGAGTCGGGCAATTTT 1103
QY 772 AGACAGATATTCAGAGGAGTATGATTTCAATCTGACCGCTGGCTTACTATCTCAGAA 831
Db 1104 CTTGGCGGTTTGAAGGCTGACCCGAGCTTTGAGAGCCCTTTGGCTTCACTCTCCC 1163
QY 832 GCTGCTAAAGATTTGATCTATAAATGCTGAAAGAGGCCCAAGAACGATTTCTGCT 891
Db 1164 GAAGCCAGGATTTCTGTAAGGCTCTCTGTAATAGGATATGCGGAAACGATGCT 1223
QY 892 CATGAAGCCTTTGTCACCCATGATTTGCGATGAACAGCAGCAGCAGCAGCCTCT 951
Db 1224 GCACAAGCTTTAATCATCCATGATTTGAGATTTGAGATTTGAGATTTGAGATTT 1277
QY 952 GATCCAGCAGCTTTATCTCTGCTTAAAGCAGTTTCTCAATGAATTAAGATTAAGAAATG 1011
Db 1278 GATATCTTAGTGTACAGACTTTGTGAGGAATTTATCTCTGTCATCATCCATGAGAAAGCT 1337
QY 1012 GATTTAGGCTTTATCTGCTAGAGACTTTTCAGAGGAGAAATTTGAGGCTCTCAAGAAATG 1071
Db 1338 GCTTTGAAGGCGCTCTCAAGACTTTTAACCGAAGCAGAGACTTTTATCTAGCTACTCAA 1397
QY 1072 TTCAAGATGATAGACACAGACAGCAGGAGAACTTTTGAAGAGCTCAAAAGCGGCT 1131
Db 1398 TTATGCTCTAGAACCAAGTAACAAGCTGCTGTTACTTTTGAATTTTCAGACAGGCA 1457
QY 1132 TTGAAGAGAGTCGGATCTGAATGATGAA 1161
Db 1458 CTGCTGAAAAAATTCACAGAGGCCATGAAA 1487

RESULT 12
US-09-938-842A-1063
; Sequence 1063, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1063
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1063

Query Match 11.5%; Score 200.6; DB 9; Length 1800;
Best Local Similarity 52.4%; Pred. No. 8.1e-36;
Matches 490; Conservative 0; Mismatches 439; Indels 6; Gaps 2;

QY 229 AATCGATCCGAGCGAAGCTGCTGTCGCGAGGATTTACGAATGATGCTGCGTGG 288
Db 526 AAAGTCATCCCAAAATCTAAGATGACATCTGCAATATCTATAGAGGATGAGAGAA 585
QY 269 ATTGATGATGATCATCTCTGATGATCCAAATGTTTGTAGGATCAAGAGGACTTAT 348
Db 586 GTGAAAATCTGCGGCTTATCTGGACATCAAAATTTGTACAAATCTATGATGCTTC 645
QY 349 GAAGATTCGGTGTGTTGTTTCATATTTGATGAGGTTTGTGAAGTGTGAGCTTTTGT 408

```

```

Db 646 GAGGACAAATGCCAACGTTTACATCGTTATGAGAGTTATGAGAGTGGTGAATCTTCTTGAC 705
QY 409 CGGATGTTTCTA---AAGTCAATTTTAGTGAAGCTGCAAGCTTCAAGCTTATTAAAGAG 465
Db 706 AGGATCTAGCAAGGAGGAAATACTCTGAAGATGATGCAAAAGCAGTCTTATACAG 765
QY 466 ATCTTGGTGTGTTGAGGCTTGTCATCTCTTGGTGTATGATGATAGAGATCTCAAACT 525
Db 766 ATCTTAAAGTCGCTAGCTTTCTGTCATCTCAAGAGGTTGTTTCATCGAGATCTAAACCA 825
QY 526 GAGAATTTCTTTGTTGATGCTTAAAGATGATGCTAAAGCTTAAAGCTTAAAGCTTAAAGCT 585
Db 826 GAGAATTTCTTTGTTGATGCTTAAAGATGATGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 885
QY 586 TTGCTGCTCTTATAGCAGGACATATTTATGACGTAGTGTGAAGTCCGCTACTAT 645
Db 886 TTATCGGACTTTGTGACAGCAGCAGAAAGACTAAATGATATAGTGGAGTGTATATTAC 945
QY 646 GTTGACACAGAGGTCTAAAGAAATGTTATGACCTCTGAAATAGATGTGTGGAGTGTGTT 705
Db 946 GTAGCCCTGAGTTCTACACAGATCTTATACACAGAGCGGATGTATGAGCATAGGA 1005
QY 706 GTTATCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCTGGCAGAGACTGAGTCTGGA 765
Db 1006 GTCATAGCATACATTTCTCTATGTGGAAGCGCTCTTTTGGCAGAGACTGAATCAGGA 1065
QY 766 ATCTTTAGACAGATTTGCAAGGGAAGTTAGATTTCAATCTGACCCGTCGCTACTATC 825
Db 1066 ATTTTCAGAGCAGTTCTAAAGCTGATCCCGATTTTGTATGAACCTCTTGGCTTCTGTTA 1125
QY 826 TCAGAGCTGTAAAGATTTGATCTATAAATGCTCAAGAGGAGCCCAAGAGAGCAGT 885
Db 1126 TCCCTTTGAGGCAAAAGATTTGTTAAGAGATTTATGTACAGAGCCCTCGGAAAGATG 1185
QY 885 TCTGCTCATGAGCCCTGTCACCCATGAGATTTCTGATGAAACAGCAGCAGCAGCAAG 945
Db 1186 ACTGATCTCAGCTTTGATGATCCCTGATCGGGTTATTA---GAAATAGATATC 1242
QY 946 CTTCTGATCCAGCAGTCTTATCTGCTTAAAGCAGTTTCTCAATGAATAGATTAAG 1005
Db 1243 CCATTTGATATTTCTGATCTTCAAGCAGATCAAGCAGATCTTGTGATCTTCTTGGC 1302
QY 1006 AAAATGGCATTCAGGTAATTTCTGATGAGACTTTTCAGAGGAGAAATTTGAGGTTCTGAAG 1065
Db 1303 AAAGCTGCTTTGATGCTCTGCAAGACATTAACCTGATGACITCTTATCTGAAA 1362
QY 1066 GAATTTTCAAGATGATAGACACAGCAACAGCGGAGAGATTTCTTTGAAGAGCTCAA 1125
Db 1363 GCGCAGTTTGCACACTTAGCACCCCAAAAATGCGCTCATCACTTTTAGATAGATCAGA 1422
QY 1126 GCGGTTTGAAGAGAGTGGATCTGAACTGATGGA 1160
Db 1423 CTGGCATTGCGACAAATGCAACAGAGCAATGAA 1457

RESULT 13
US-09-938-842A-3678
; Sequence 3678, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1063
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1063

```

; PRIOR APPLICATION NUMBER: US 60/300,111  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 3678  
; LENGTH: 718  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-3678

Query Match 11.0%; Score 193; DB 9; Length 718;  
Best Local Similarity 100.0%; Pred. No. 2.8e-34;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CTCATCATCTTCCACATTTCTGTTTTTTTCTCTTAAATTCGTTTATATTTGAAT 1614  
DB 1 CTCATCATCTTCCAAATTTCTGTTTTTTTCTCTTAAATTCGTTTATATTTGAAT 60  
QY 1615 CTAATTTCTAAGGATACAAAATATATTTCTGGCTGTTTTTCTTTCCTTTTATTTT 1674  
DB 61 CTAATTTCTAAGGATACAAAATATATTTCTGGCTGTTTTTCTTTCCTTTTATTTT 120  
QY 1675 GTACATGAGCACTTCTAAATTTTATCTCTCATATGATAATTTTGTCTCATATAAAA 1734  
DB 121 GTACATGAGCACTTCTAAATTTTATCTCTCATATGATAATTTTGTCTCATATAAAA 180  
QY 1735 GTTTTGAATCC 1747  
DB 181 GTTTTGAATCC 193

RESULT 14  
US-09-854-731-3  
; Sequence 3, Application US/09854731  
; Patent No. US20020120949A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 2374  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-854-731-3

Query Match 10.9%; Score 189.6; DB 10; Length 2374;  
Best Local Similarity 53.8%; Pred. No. 2.7e-33;  
Matches 440; Conservative 0; Mismatches 369; Indels 9; Gaps 2;

QY 271 GAAGATGATGCGGTGAGATTCAGATCATGTCATCTCTGAGCATCCAAATGTTGT 330  
DB 846 GAGGATGTTGTAGAGAGTAAATTTTGAAGCGTTATCAGGCGCAATAATCTCGTC 905  
QY 331 AGGATCAAGAGGACTTATCAAGATTCGGTGTGTTGTTTCATATTTGTTAGAGGTTTGTGAA 330  
DB 906 AAATTTCTATGATGTCATGTGAGATGGCTCAATGTCATATTTGTCATGGAATTATGTGAG 965  
QY 391 GTGTGTGAGCTTTTGTAGCGATGTTTCTAAAGTCAATTTTAGTGAGCGTGAAGCTGTC 450  
DB 966 GGAGGAGAAATTCCTAGACAGAAATATATAGCCAGAGCGGGAGATACACAGAGGAAGATGCC 1025  
QY 451 AA---GCTTATTAACAGCATTTCTGGTGTGTTGTTGAGGCTTGTCATTTCTTGTGTTATG 507  
DB 1025 AAAGCGAATTTGTACAGATTTTGAAGCGTAGTAGCCITCTGTCATCTCAGGGGTAGTG 1085  
QY 509 CATAGAGATCTCAAACTGAGAAATTTCTTGTGTTGATGTCCTAAAGATGATGCTAAGCTT 567

DB 1086 CATCGTGATTTGAAGCCAGAGAAATTTCCCTTTTCAACACCGAGGATGAATAATGCTCCCATG 1145  
QY 568 AAGCTACCGATTTTGGTTTGTCTCTCTATATAAGCCAGGACAATATTTATATGACGTA 627  
DB 1146 AAGTTGATTTGTTGTTCTCTCTGATTTCAITAGAACAGATGAAAGGCTTAATGATATT 1205  
QY 628 GTTGGAAAGTCCGTACTATGTTGACCCAGAGGTGCTAAAGAAATGTTATGACCTGAAATA 687  
DB 1206 GTTGGAAAGTGCATATATGTTGCCAGAGGTTTTCACAGATCATATAGTATGAGACA 1265  
QY 688 GATGTGGAGTGTGTTTATCTCTCTACATTTTACTCAGCGGTGTTCTCTCCCTCTGG 747  
DB 1266 GACATTTGGAGTATAGTGTGCATAAAGTACATTTCTGCTCTGTGGCAGTCGGCAATCTCG 1325  
QY 748 GCAGAGACTGAGTCTGGAATCTTTAGACAGATATTTCAGAGGAAGTTAGATTTCAATCT 807  
DB 1326 GCAGAAACAGAAATCAGGAATATTCAGATCTGTTGAGAGCTGATCCCAACTTTTGATGAT 1385  
QY 808 GACCGTGGGCTTACTATCTCAGAAAGCTGTCTAAAGATTTGATCTATAAAATGCTCGAAAG 867  
DB 1386 TCACCGTGGCTACAGTATCAGCTGAAGCTAAGGATTTTGTGAAGAGATTTCTGAACAAA 1445  
QY 868 AGCCCAAGAAAGCATTTCTGCTCATGAAGCCTTGTGTCAACCATGGATTGTCATGAA 927  
DB 1446 GATTACCGCAAAAGAAATGACCGCTGTTCAGACACTGACTCATCTTGGTTGCGAGATGAA 1505  
QY 928 CAAGCAGCACCGACAGAACGCTTTGATCCAGCAGTCTTATCTGCTCTAAAGCAGATTTTCT 987  
DB 1506 CA-----AGGCAGATCCCGCTGGACATCATCTTCAGATTAATTAAGCAATACCTC 1559  
QY 988 CAAATGAATAGATTAAGAAATAGGATTTACGGGTAAATTTGCTGAGAGACTTTTCAGAGGAA 1047  
DB 1560 CGCGCTACAGCTCTTAAACGGTTGGCATTTAAAGGCACTATCCAAAGGCTTTAAGGGAAGAT 1619  
QY 1048 GAAATTGAGGCTCTGAAGGAATTTTCAAGATGATAGA 1085  
DB 1620 GAACTTTGTATCTCAAACTGCGAGTTTAACTGCTCGA 1657

RESULT 15  
US-09-878-574-3809  
; Sequence 3809, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 3809  
; LENGTH: 413  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-005-Q1-B1-B8  
US-09-878-574-3809

Query Match 9.6%; Score 168; DB 10; Length 413;  
Best Local Similarity 63.2%; Pred. No. 9.5e-29;  
Matches 258; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 834 TGCTAAAGATTTGATCTATAAAATGCTCGAAAGAGGCCCAAGAAACGCAATTTCTGCTCA 893  
DB 4 TGCTAAAGACCTAGTCAGGAAGATGCTGACACAGGATCCAAACAGCGGATTAATCTTCTC 63  
QY 894 TGAAGCCTTGTGTCACCATGGAATGTCGATGAACAGCAGCAGACAGCAAGCCTTTGA 953  
DB 64 TCAAGTCTTTGAACACCCATGGATGAGAGAAGGTGAGATGTCATCTGATAAACCAATCGA 123

QY 954 TCCAGAGCTTATCTCTCTAAGCAGTTTTCTCAAATGAATTAAGATTAAAGAAATGGC 1013  
Db 124 TAGTGCAGTTCTATCCAGAATGAACAATTCAGGGCATTGATTAAGCTCAAGAGCTAGC 183  
QY 1014 ATTACGGGTAATTGTGTGAGAGACTTTCAGAGAAAGAAATTCGAGGCTCTGAAGGAATGTT 1073  
Db 184 AATTGAAGGTTATCGCTGAAAATCTATCAGAAGAGGAGATTAAAGGTTCTCAAAGCAATGTT 243  
QY 1074 CAAGATGATAGACACAGACAAACAGCGGAAACGATTACTTTTGAAGAGCTCAAAGCGGTTT 1133  
Db 244 TGCCAACTGGGACACTGACATATAGTGGCATTATCACCTATGAGAATTAAGACTGSCIT 303  
QY 1134 GAAGAGAGTCGGATCTGAAGTCTGATGGAATCAGAAATCAAGTCTCTCATGATGGGCTGA 1193  
Db 304 GGCTCGAATCGGATCAAAACTGCTGAGGCTGAAGTGAAGCAACTCATGGATGGGCTGA 363  
QY 1194 TATCGACACAGTGGTACAAATAGACTACGGAGAAATTCCTAGCAGCAAC 1241  
Db 364 TGTGACGGAAATGGGTGATTGACTATCTTGAATTCATTTCCGGGTAC 411

Search completed: February 13, 2003, 21:08:05  
Job time : 110 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2003, 17:42:17 ; Search time 2587 Seconds

(without alignments)  
10936.805 Million cell updates/sec

Title: US-09-848-806-2

Perfect score: 1747

Sequence: 1 gatccgggacatattctc.....tataaaagtgttgattcc 1747

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estm:\*

5: em\_estov:\*

6: em\_estopl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	598	34.2	2380	11	AY109473 Zea mays
2	563.4	32.2	591	10	AV825282 AV825282
3	523.6	30.0	2566	11	AY109374 Zea mays
4	505.8	29.0	2298	11	AY109401 Zea mays
5	503.8	28.8	507	10	AV558412 AV558412
6	484	27.7	835	12	BG647837 EST509456

c	7	480.6	27.5	1628	11	AY109463
c	8	466.8	26.7	814	12	BG887873 EST513724
c	9	439	25.1	493	17	B28263 TSA20TFB TA
c	10	437.8	25.1	1087	17	B11596 TSA20-T7 TA
	11	424.8	24.3	528	9	A1994248 701501524
	12	418	23.9	742	12	BG596613 EST495291
	13	402.4	23.0	813	14	BM779035 EST589610
	14	401.8	23.0	686	13	B1178776 EST519721
	15	388.8	22.3	751	14	BQ863474 QRC5A16 Y
	16	379.2	21.7	723	14	BQ986998 QRC5A16 Y
	17	375.8	21.5	635	10	AW587489 IPFGH2007
	18	374.2	21.4	695	14	BQ115699 EST601275
c	19	374	21.4	421	10	AV790851 AV790851
	20	374	21.4	777	14	BQ990683 QGP20K08
	21	372.6	21.3	689	14	BQ506885 EST614300
	22	371.4	21.3	697	13	B3302783 B3302783
	23	370.6	21.2	673	14	BQ248574 TRB15008D
	24	361.2	20.7	713	14	BQ801121 WHE2810 E
	25	355.2	20.3	727	14	BQ765867 EBR003 SQ
	26	353.6	20.2	918	14	BM817364 HC107G07
	27	352	20.1	650	12	BQ423173 GA_EA001
	28	351.6	20.1	635	10	AW011661 614011E01
	29	347.6	19.9	683	14	BQ005844 QCG9D23 Y
	30	347	19.9	748	14	BQ967112 QHB28R17
	31	344.6	19.7	611	13	B1178918 EST513951
	32	342.8	19.6	700	9	AL506058 AL506058
	33	341.4	19.5	625	13	BQ245960 BJ245960
	34	340.4	19.5	737	14	BQ969859 QHB39L22
	35	340.4	19.5	750	14	BQ916638 QHB18118
	36	339.8	19.5	747	14	BQ970309 QHB41K23
	37	338.2	19.4	635	10	AV925405 AV925405
	38	335.2	19.2	673	14	BQ865634 QCG5102 Y
	39	331	18.9	612	13	B1074799 IPI_16_H1
	40	330.4	18.9	554	9	A1894480 EST363523
	41	329.4	18.9	740	12	BG233877 sab50409
	42	324	18.5	682	13	BQ292898 BJ292898
	43	322.8	18.5	698	12	BQ592594 EST491672
	44	322.6	18.5	584	9	AI162867 A025P73U
	45	322.4	18.5	658	10	AV914419 AV914419

ALIGNMENTS

RESULT 1	AY109473	2380 bp	linear	HTC 25-MAY-2002
LOCUS	AY109473			
DEFINITION	Zea mays CUI905_1 mRNA sequence.			
ACCESSION	AY109473			
VERSION	AY109473.1			
KEYWORDS	HTC			
SOURCE	Zea mays.			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.			
AUTHORS	Hayney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.			
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes			
JOURNAL	Unpublished (2002)			
REFERENCE	2 (bases 1 to 2380)			
AUTHORS	Coe,E.C.			
TITLE	Direct Submission			
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA			
FEATURES	Location/Qualifiers			
source	1..2380			
	/organism="Zea mays"			
	/db_xref="MaizeDB:630671"			
	/db_xref="taxon:4577"			
	/clone="CUI905_1"			





```
QY 791 AGTTAGATTTCATATCTGACCCGTGGCTACTATCTCAGAGCTGCTAAAGATTGATCT 850
Db 1418 GCTCGACTTCAGTTCGAGCGGTGGCCAGCACTCCGACGGCCCAAGGATCTCGTGA 1477
QY 851 ATAAATGCTGAAAGGAGCCCAAGAAACGATTTCTGCTCATGAAGCCCTTGTGTCACC 910
Db 1478 GGAGGATGCTTCTCAGGACCCGAGGAAGAGACTGACCGCTCAGGAAGTCTCAGGCATC 1537
QY 911 CATGATTTCGATGAACAAGCAGCAGCAGCAAGCCCTTCCTGATCCAGCAGTCTTATCTC 970
Db 1538 CTGAGGTCAGTCTGAGTGGTCTCTGACAGCCGCTGAGCTCGCCGCTTGTGCTC 1597
QY 971 GTCTAAGCAGTTTCTCMAATGAATAGATTAAGAAATGCGATACGGTAAATTCCTG 1030
Db 1598 GCATGAAGCAGTTCTCGGCTATGAATGAAGCTGAAGAGATGGCTCTTAGGGTGAATCCCG 1657
QY 1031 AGAGACTTTTCAGAGGAAGAAATTCGAGGTCTGAAGAAATTTTCAAGATGATAGACACAG 1090
Db 1658 AGAACCTGTGAGAGGAGAGATCGCCGGCTGAGGAGATGTTCAAGATGATCGACGCG 1717
QY 1091 ACAACAGCGGAACGATTTCTTTGAAGAGCTCAAAAGCGGTTTGAAGAGTCTGATCTG 1150
Db 1718 ACAACAGCGGCGAGATCACGTTTCGAGGAGCTCAAGGTTTGGCTCGAGAGAGTGGCGCCA 1777
QY 1151 AACTGATGAATCAGAAATCAAGTCTCTCATGATCGCGCTGATATCGACAACAGTGTGA 1210
Db 1778 ACCTGAGAGTCTGAGATCTACGCGCTCATGCAAGCGCGGAGCTGCAACAACAGCGCA 1837
QY 1211 CAATAGACTACGAGAAATTCCTAGCAGCAACCTTACATGAAAGATGAGAGAGAGG 1270
Db 1838 CGATCGACTACGCGAGTTTCATCGCGCCACGCTGCACCTGAACAAAGGTGAGCGGGAGG 1897
QY 1271 AGATTCTGGTGGTGCATTTTCGAGCTTTGCAAGAGCGGAGCGGTTATATCAACATCG 1330
Db 1898 ACCACCTGTTTCGCGGCTCCAGTACTTCGACAGAGCGGACGCGGNNNNNNNNNNNN 1957
QY 1331 ATGAGCTTACGTCAGCTTGCACAGAGTTTGGTCTATGATACACCTCTGACGACATGA 1390
Db 1958 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2017
QY 1391 TCAAGGAGATGATCTTGACAAACGCGGAAGATCGATTCTCGGAGTTTACAGCAATGA 1450
Db 2018 TCGGGGAAGTCGACAGCAACAGCGGGGCGCATAGACTACACAGATTCGTGGCGATGA 2077
QY 1451 TGAGGAA 1457
Db 2078 TGCAGAA 2084

RESULT 4
LOCUS AY109401 2298 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays CL1577_1 mRNA sequence.
ACCESSION AY109401
VERSION AY109401.1 GI:21213112
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE 1. (bases 1 to 2298)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
JOURNAL Overgo Probes
REFERENCE 2. (bases 1 to 2298)
AUTHORS Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES Location/Qualifiers
```

```
source 1. 2298
/organism="Zea mays"
/db_xref="MaizeDB:630430"
/db_xref="taxon:4577"
/clone="CL1577_1"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT 544 a 464 c 597 g 524 t 169 others
ORIGIN
Query Match 29.0%; Score 505.8; DB 11; Length 2298;
Best Local Similarity 61.8%; Pred. No. 9.9e-83;
Matches 817; Conservative 0; Mismatches 502; Indels 3; Gaps 1;
QY 142 TACCTTCTGGGAAAAAGCTAGGCCAAGGGCAATTTGGAAACAACCTATCTCTGCACAGAG 201
Db 666 TACTCCTTCGGAGGAGCTTGGCCGGGCCAGTTCCGGGTGACATACCTCTGCACAGAG 725
QY 202 AAATCAACTCCGCTTAATAGCCTTGCATTCGATCCGGAAGCGAAGCTCGTGTGCGC 261
Db 726 GTTGCTCTGGGAGGACGTAGCCTTCAAGTCCATCTCCAAGCGCAAGCTCGCCAGCAAG 785
QY 262 GAGGATTACGAGATGTATGCGGTGAGATTCAGATCATGATCATCTCTCTGAGCATCCA 321
Db 786 GCAGACAGGAGGACATTCGAAAGGAGATTCAGATCATGAGCACCTGTCTGGGACCCA 845
QY 322 AATGTTGTAGGATCAAAAGGACCTTATGAAGTTCCGGTGTGTTGTTCAATTTGTTATGGAG 381
Db 846 AACATTGTCAGTTCCGGGAGCATACGAGGACAAGACAATGTCCATGTGGTGAAGAG 905
QY 382 GTTGTGAAGTGTGGTGTGATTTTTCATCGGATTTCTTAAAGTCAATTTAGTGACCGT 441
Db 906 CTCTGCGCAGGTGGGAGCTCTTCATCGCATCATTCGCAAGGGGCTACACAGAGCGT 965
QY 442 GAAGCTGTCAAGCTTTAATGAACGATTTCTGTTGTGTGAGGCTTGTCAATCTCTCTGTT 501
Db 966 CGCGCTGCTACAATCTGCAGAGCAGTTGTGAATGTGTCAACATTTGCCACTTCATGGGT 1025
QY 502 GTTATGCATAGAGATCTCAAACTTCAGATTTCTTGTGATGATCTCTTAAGATGATGCT 561
Db 1026 GTGATCACCGTCACTGAAACCGGAGAACTTTCTGTTGCGACCAAGGAGGAAATGCA 1085
QY 562 AAGCTTAAGGCTACCGATTTTGGTGTGTCTTCTTCTATAAGCCAGGACAATATTTATAT 621
Db 1086 ATGCTCAAGGCCACCTGATTTTGGGCTTTCCGTTTCATCGAAGAAAGAAAGATGTACAGG 1145
QY 622 GAGTAGTTGGAAGTCCGCTACTATGTTGCACAGAGGTCTTAAGAAATGTTATGGACCT 681
Db 1146 GACATCGTTGGAAGTCTTATTTATGTTGGCTGAACTTCTTAAGCGGAGCTATGGAAA 1205
QY 682 GAAATAGATGTGGAGTCTGCTGTGTTATCTCTCATATTTTACTCAGCGGTGTTCTCTCC 741
Db 1206 GAGATAGATTTGGAGCCAGGTGTTATTTTGTACATTTCTTCTCAGTGTGTGCTCCA 1265
QY 742 TTTGCGGACAGACTGAGTCTGGAAATCTTTAGACAGATTTGCAAGGAGGATGATTTTC 801
Db 1266 TTTTGGGCTGAAATTTGAAAAGGGGATTTTGTATGTTCTGATGAGGAGATGACTTT 1325
QY 802 AATCTGACCGTGGCTACTATCTCAGAGCTGCTAAAGATTTTGTATCTATAAATGCTC 861
Db 1326 GAAAGTCAACTTTGGCCATCAATTTCTGAGAGTCTTAAGACTTGTGTAGAAAGATGTTG 1385
QY 862 GAAAGGAGCCCCAAGAAACGATTTCTGCTCATGAGCCCTGTGTCAACCCATGGATTGTC 921
Db 1386 ACAGGAGTCCAAAGAAAGAGACTGACTTCAGCTCAAGTTCTTCAACATTCATGGCTCAGA 1445
QY 922 GATGACAAGCAGCACCAAGCAAGCCCTTTGATCCAGGAGTCTTTATCTCGTTAAAGCAG 981
```

```

Db 1446 GAAGTGGAGGTGATCTGATGATGAGCTTATGATGAGTCTGTTCTTTCTAGATGAAGCAG 1505
QY 982 TTTTCTCAATGAATGAATTAAGAAATGCGATTACGGGTAAATGCTGAGAGACTTTCA 1041
Db 1506 TTCAGAGCAATGAATGAGCTGNNNNNGATGGCCCTAAAGTTATTGCTCAACCTTAAC 1565
QY 1042 GAGGAAGAAATGAGGTCTCAAGGAATTTGTCAGAGATGATAGACAGACAAACAGCGGA 1101
Db 1566 GAGGAAGAGATCAAGGGGCTAAAGCAATGTTTCATGAACATGGACAGACAAATAGTGGC 1625
QY 1102 ACGATTACTTTTGAAGAGCTCAAGAGCGGTTTGAAGAGATGCGATCTGAATGATGGA 1161
Db 1626 ACAATCAATATGAAGAACTCAAGAGAGATTAGCCAACTTGGATCAAGCTGTGAGAA 1685
QY 1162 TCAGAAATCAAGTCTCTCATGATGCGGTGATATGCAACAGAGTGTGATCAATAGACTAC 1221
Db 1686 GCTGAAGTAAAGCAGTGTGATGAGGCTGCTGATGTTGATGGAATGATCTATTGACTAT 1745
QY 1222 GGAGATTCCTAGCAGCACTTACACATGAACAAGATGAGAGAGAGATCTGTTG 1281
Db 1746 GTTGAGTTCATCTGCTGACCAATGATAGACAAAGCTCGAAAGGAGAGATTTGTTT 1805
QY 1282 GCTGCAATTTTCGGAATTTGCAAAAGACGAGCGGTTATATCACCATCGATGAGCTTCAG 1341
Db 1806 AAGGCAATCCAGTCTTTGACAAAGATAACAGCGCTTCATCAACAGGATGAATGGAA 1865
QY 1342 TCAGTTCCACAGAGTTTGGTCTATGATGATAC---ACCTCGAGCAGATGATCAGGAG 1398
Db 1866 TGTGTTTGTGATGAGTATGATGAGTGGGACAGAGTCAATAAAGGAGATCATATCAGAA 1925
QY 1399 ATTGATCTTGACATGACGGGAAGATGATTTCTCGGAGTTTACAGCAATGATGAGGAAA 1458
Db 1926 GTTGACAGATATGATGAGGAGATTAATCTATGAGGAGTTTGTGCAATGATGAGAGGA 1985
QY 1459 GG 1460
Db 1986 GG 1987

```

```

RESULT 5
AV558412/c AV558412 507 bp mRNA linear EST 07-SEP-2000
LOCUS AV558412 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ098B02F 3', mRNA sequence.
ACCESSION AV558412
VERSION AV558412.1 GI:8729838
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 507)
ASAMIZU, E., NAKAMURA, Y., SATO, S. and TABATA, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..507
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="caxon:3702"
/clone="SQ098B02F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
FEATURES
source

```

```

/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 179 a 104 c 80 g 144 t
ORIGIN
Query Match 28.8%; Score 503.9; DB 10; Length 507;
Best Local Similarity 99.8%; Pred. No. 3.6e-82;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1241 CCTTACACATCAACAAGATGGAGAGAGAGATTCCTGGTGGCTGCATTTTCGGACTTTG 1300
Db 507 CCTTACACATCAACAAGATGGAGAGAGAGAGATTCCTGGTGGCTGCATTTTCGTACTTTG 448
QY 1301 ACAAGAGAGAGAGAGAGAGATTCACCATGATGAGTTCAGTCAGCTTCACAGAGTTTG 1360
Db 447 ACAAGAGAGAGAGAGAGATTCACCATGATGAGTTCAGTCAGCTTCACAGAGTTTG 388
QY 1361 GTCTATGTGATACACCTCTCGAGAGAGATTCATCAAGAGAGATTCATCTTGACAATGACGGA 1420
Db 387 GTCTATGTGATACACCTCTCGAGAGAGATTCATCAAGAGAGATTCATCTTGACAATGACGGA 328
QY 1421 AGATCGATTTCTCGAGATTTACAGCAATGATGAGGAAGAGATGAGTTGGAGAGCA 1480
Db 327 AGATCGATTTCTCGAGATTTACAGCAATGATGAGGAAGAGATGAGTTGGAGAGCA 268
QY 1481 GAACCATGATGAAGAACTTCGAACCTTCAACATTCCTGATGCTTTTGAGTTGATGTA 1540
Db 267 GAACCATGATGAAGAACTTCGAACCTTCAACATTCCTGATGCTTTTGAGTTGATGTA 208
QY 1541 AATCGATGATGATCATCATCTTCTCCCAATTCCTGTTTTTTTCTCTTAATTCCT 1600
Db 207 AATCGATGATGATCATCATCTTCTCCCAATTCCTGTTTTTTTCTCTTAATTCCT 148
QY 1601 TTATATTTCGAATTCGAATTTCTAAGGATACAAATATATCTGCTTGTGTTTGTGCTT 1660
Db 147 TTATATTTCGAATTCGAATTTCTAAGGATACAAATATATCTGCTTGTGTTTGTGCTT 88
QY 1661 TCCTTTTATTTTGTACATGAGCAACTTTCTAAATTTTATCCTCATATGATAATTTT 1720
Db 87 TCCTTTTATTTTGTACATGAGCAACTTTCTAAATTTTATCCTCATATGATAATTTT 28
QY 1721 TGCTTCATATAAAGTTTTTGAATTC 1747
Db 27 TGCTTCATATAAAGTTTTTGAATTC 1
RESULT 6
BG647837 835 bp mRNA linear EST 24-APR-2001
LOCUS BG647837 HOGA Medicago truncatula cDNA clone PHOGA-18E5 5' end,
DEFINITION mRNA sequence.
ACCESSION BG647837
VERSION BG647837.1 GI:13782949
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
JOURNAL Medicago.
COMMENT 1 (bases 1 to 835)
Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,
Uterback, T., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
Unpublished (2001)
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu

```

G391443e TIGR sequence name: MTMCE27TK More information is available at: www.medicago.org  
Seq primer: SKMD CTA GGA CTA gtg GAT CC).

## FEATURES

Location/Qualifiers  
1..835  
/organism="Medicago truncatula"  
/cultivar="A17"  
/db\_xref="taxon:3880"  
/clone="PHOGA-19E5"  
/clone\_lib="HOGA"  
/tissue\_type="3 day old seedling roots"  
/dev\_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"  
/lab\_hosts="XILOR"  
/note="Vector: paluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."  
230 a 137 c 210 g 258 t

## BASE COUNT

230 a

## ORIGIN

Query Match 27.7%; Score 484; DB 12; Length 835;  
Best Local Similarity 75.2%; Pred. No. 1.3e-78;  
Matches 629; Conservative 0; Mismatches 205; Indels 2; Gaps 2;  
QY 406 GATCGAATTTCTTAAAGGTCATTTAGTGGCGTGAAGCTGTCAAGCTTATTAGAAG 465  
DB 2 GATATGATGTCCAGAAAGGCGATTATAGTGAGACAAAGCTGTAAGTTGATTAGA 61  
QY 466 ATCTCTGTTGTTTGAGGCTTGTCAATCTCTTGGTGTATGCATAGATCACAACCT 525  
DB 62 ATTGTGAGGTTTGAAGCTTGTCAATCTCTTGGTGTATGCATAGATCACAACCT 121  
QY 526 GAGAAATTTCTTGTGATAGTCTCTAAAGATGATGCTTAAGCTTAAGGCTACCGA 585  
DB 122 GAGAAATTTCTTGTGATAGTCTCTAAAGATGATGCTTCTCAAACTATTGATT 181  
QY 586 TTGCTCTGTTCTTAAGCCAGACAAATTTATATGACGTAGTTGAGTCCGTACTAT 645  
DB 182 TTGCTCTGTTTTCACAGCCAGGTGAAATCTTTAGTGTGTTTGGAGCCCATAT 241  
QY 646 GTTGCCACAGAGTGTCTAAAGAAATGTTATGACCTGAATAGATGTGGAGTGGT 705  
DB 242 GTTGCCACAGAGTGTCTGACAAATATGACCTGAACGACGTGTGGAGTGGT 301  
QY 706 GTTATCCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCGGCGAGACTGACTTGA 765  
DB 302 GTTATTTTGTACATCTTATTAAGCGGGTGCCTCGGTTTGGCGGAGACGATCA 361  
QY 766 ATCTTTAGACAGATATTGCAAGGAGTGTAGATTTCAAATCTGACCGTGGCTACTAT 825  
DB 362 ATCTTCAGACAGATTTTCCAGGAAACTTGTATTTCCGCTGTGACCGTGGCTGG 421  
QY 826 TCAGAAAGTCTTAAAGATTGTATCTATAAAATGCTCGAAAGAGGCCCAAGAACG 885  
DB 422 TCAGACAGTGCACAGGATCTAATTCGAAATAATGCTTGTATAGGAACCCAAAT 481  
QY 886 TCTGCTCATGAGCCCTTGTCTACCCATGATTTGCTGATGAACAAGACGACGACA 945  
DB 482 ACAGCTCACCAAGTCTGTCTACCCGTTGATTTGATGATTAATTCACCATGATA 541  
QY 946 CTTCTTATCCAGCAGTCTTATCTCTCTTAAAGCAGTTTCTCAATGAATGAATTA 1005  
DB 542 CTTCTTATCTGCTGTTTATCTCGCTGAAGCAGTCTCTGCGATGAATAAACTTAA 601  
QY 1006 ABAATGCAATAGGGTAATGCTGAGAGACTTTCAGAGGAGAAATGGAGTCTGAAG 1065  
DB 602 AAGATGCTTTACGTGTTATTGGGAGAGGCTTCTTGAGAGAAATTTGGTGGTTGA 661

QY 1066 GAATTTGTTCAAGATGATAGACACAGACAAACGCGGAAACGATTACTTTTGAAGAGCTCAA 1125  
DB 662 GAGTATTTCAGGATGCTTGTATGCTGATAATAGTGGAACTATACATTGGGAGAGTTAAA 721  
QY 1126 GCGGTTTGAAGAGATCGGATCTGAACCTGATGGAATCAGAATCAAGTCTCTCATGGAT 1185  
DB 722 GAAGCTTAAAGCGAGTAGGATCTGAACCTTATGGAGTCTG-AATCAAGGATCTTATGGAT 780  
QY 1186 GCGGCTGATATCGACAAACAGTGTGTAACAATAGACTACGGAGAAATTCCTAGCACAAC 1241  
DB 781 GCAGCAGATATAGATTATA-CGGGACACTTGACTATGGGAAATTCATTGCTGCTAC 835

## RESULT 7

AY109463/c 1628 bp mRNA linear HTC 25-MAY-2002

DEFINITION Zea mays CL10776\_2 mRNA sequence.

ACCESSION AY109463

VERSION AY109463.1 GI:21213192

KEYWORDS HTC

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1628)

AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of

JOURNAL Overgo Probes

REFERENCE 2 (bases 1 to 1628)

AUTHORS

Coe, E.C.

TITLE Direct Submission

JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of

MISSOURI, Columbia, MO 65211, USA

FEATURES

source

1..1628

/organism="Zea mays"

/db\_xref="MaizeDB:629956"

/db\_xref="taxon:4577"

/clone="CL10776.2"

/clone\_lib="Maize Mapping Project/DuPont Consensus

Library"

/notes="this sequence is part of a project of EST

assemblies resulting from the application of public

contigs to seed DuPont contigs; this resource was

assembled by DuPont as part of a collaboration for the

overgo addressing of BACs in conjunction with the Maize

Mapping Project"

BASE COUNT 393 a 408 c 350 g 424 t 53 others

ORIGIN

Query Match 27.5%; Score 480.6; DB 11; Length 1628;

Best Local Similarity 60.0%; Pred. No. 4.3e-78;

Matches 775; Conservative 0; Mismatches 514; Indels 3; Gaps 1;

QY 169 GCCCAATTGGAAACCACTATCTGACACAGAGAAATCAACCTCCGCTAATTACGCTGC 228

DB 1615 GCCCCAGTCGGGGTCACTCTGTCAGGCCTCGGAGACCGGGAGCGCTTCGCTGC 1556

QY 229 AAATCGATCCCGAAGCAAGCTGTGTGTCGAGGATTACGAAGATGTATGCGGTGAG 288

DB 1555 AAGTCATCGCCACCGGAAGCTGTCCACCGGACGACATTGAGGACGTGCGCGGGAG 1496

QY 289 ATTCAATCATCATCATCTCTCTGAGCATCCAATGTTTGTAGGATCAAGGACTTAT 348

DB 1495 GTGCGATCATGACCACTCACGGGCCACCGNNNNNCGTCGAGCTCCGGGAGCATAC 1436

QY 349 GAAGATTCGGTGTGTTTCATATTGTTATGAGGTTTGTGAAGTGGTGGCTTTTGTAT 408

DB 1435 GAGGACAGCACTCGGTCAACTTGTATGAGCTCTCGAGGCGGGGAGCTCTTCGAC 1376

```
QY 409 CGGATTGTTCTAAAGTGCTATTTAGTGAGCGGTGAGCTGCTCAAGCTTATTTAAGACGATT 468
Db 1375 CGCATCATAGCAAGGCGCCATACACGAGCGNNNNNNNNNNNNNNNNNNNNNNNNNGATC 1316
QY 469 CTTGTGTGTTGAGGCTTGTCATCTCTCTGGTGTATATGATAGAGATCTCAAAACCTGAG 528
Db 1315 GTGCGCGTCGTCACAGCTGCCACTCCATNNNNNTCTTCATCGGATCTCAAGCCCGAG 1256
QY 529 AATTCTCTGTTGATGCTCTAAAGATGATGCTAAAGCTTAAGCTACCGATTTTGGTTTG 588
Db 1255 AACTCTCTGTTGCTCAATAACAAGAGGAGCTCCCGCTCAAGGCCACGGACTTCGGTCTC 1196
QY 589 TCTGTCTCTTAAGCCAGGACATATTTATATGACGTAGCTGCGAAGTCCGACTATGTT 648
Db 1195 TCGTCTCTTCACAGCAGGAGACGTTTAAGATCTTGTGGAAAGTCATATATGTT 1136
QY 649 GCACAGAGGTCTAAAGAAATGTTTGGACCTGAATAGATGTTGGAGTCTGGTGT 708
Db 1135 GCTCCTGAGGTACTGAACGGAATATGGGCGAGAGGCTGACATATGGAGTCTGGGGTC 1076
QY 709 ATCCTCTACATTTTACTCAGCGGTGTTCTCCCTCTCGGCGAGAGCTGAGTCTGAATC 768
Db 1075 ATTCTTACNNNNNNNNCTGGTGTCTCTCTCTTCTGGGCGAGAGATGAGGATGGCATA 1016
QY 769 TTTAGACAGATATTTCAAGGGAAGTTAGATTTCAAAATCTGACCGGTGGCTACTATCTCA 828
Db 1015 TTTGATGCTGTCTTGGCGGTCAATCGATTTCTCTCTGACCTTGGCTTCAATATCC 956
QY 829 GAAGCTCTAAAGATTTGATCTATAAATCTCGAAGAGGCCCAAGAAAGCATTTCT 888
Db 955 AATGTCGAAGGATTTGGTTAAGAGATCTCGCAAGACCCAAAGAACGCTGACT 896
QY 889 GCTCATGAAGCTTGTGTCACCCATGATTTGTCGATGAACAGCACACAGCAAGCT 948
Db 895 GCTGCTGAATTTTGAACCCATCCATGATTTAGAGAGATGAGAGGCCCAAGATAGCCA 836
QY 949 CTTGATCCAGAGCTTTATCTGCTTAAGCACTTTTCTCAATGAATGAATTAAGAA 1008
Db 835 CTTGACATTTACTGTCATTTGTTAGAAATGAACAGTTGAGGCAATGAACAGCTCAAGAA 776
QY 1009 ATGGCATTAAGGTTAATTTGCTGAGAGACTTTGAGAGAGAAATTTGAGGCTCGAAGAA 1068
Db 775 GTTGCAITGAAGTTGTGGCTGAGACTTATCATGATGAAGAGATTAAGGCTTAAAGAA 716
QY 1069 TTGTTAAGATGATAGACACAGACAGCGGAACGATTTTGAAGAGCTCAAGCG 1128
Db 715 ATGTTCAAGTCCCTGGATACAGATAACAGTGGGACAAATTAATCTTGAAGAGCTAAGATCT 656
QY 1129 GGTGTTGAAGAGTCGGATCTGAAGTGGATGAGATCAAGTCTCTCATGATCGG 1188
Db 655 GGTTCACCAAACTTGATCTAAATTTCTGAATCAGAAATTAACAAATGATGAGGCG 596
QY 1189 GCTGATATCGAACACAGTGTGTAACAATAGACTACGAGAAATTTCTAGCAGCAACCTTACAC 1248
Db 595 GCTGATGTTGATGGAATGTTGATCAATGATTTGCGGAGTTTATATACGCCACATGAT 536
QY 1249 ATGACAAAGATGAGAGAGAGAGATCTGGTGGCTGCAATTTTGGAGCTTTGACAAAGAC 1308
Db 535 TTGAATAGATTGAGAGAGGAGAGCCACATCTACTCAAGCTTTTGAATATTTGATAGGAT 476
QY 1309 GGAAGCGGTTTATATCACCATCGATGAGCTTCAGTACGTTGACAGAGTTTGGTCT---A 1365
Db 475 CACAGCGGATACATAACCGTAGATGATTTGGAAGAGCTTTGAGAGATGATATGGGA 416
QY 1366 TGTGATACCTCTGGACGACATGNTCAGGAGATGATCTTGGACAAATGACGGGAGATC 1425
Db 415 GATGACAAAACATAAAAGAAATCATTTGCTGAGATGATACAGATCATGATGGAAGAT 356
QY 1426 GATTTCTCGGAGTTTACAGCAATGATGAGAA 1457
Db 355 AATTACAGGAGTTTGTGGCATGATGAGAA 324
```

```
RESULT 8
BG887873
LOCUS
DEFINITION
      814 bp mRNA linear EST 30-MAY-2001
      EST513724 cSTD Solanum tuberosum cDNA clone cSTD7P13 5' sequence,
      mRNA sequence.
ACCESSION
BG887873
VERSION
BG887873.1 GI:14264959
KEYWORDS
EST.
SOURCE
      potato.
      Solanum tuberosum
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
REFERENCE
      1 (bases 1 to 814)
      van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A.,
      Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
      Generations of ESTs from dormant potato tubers
      Unpublished (2001)
      Contact: Cathy Ronning
      The Institute for Genomic Research
      For clone info: please contact Research Genetics, Libraries
      Division tel 1-800-711-6195, email cdna@resgen.com
      Seq primer: M13F-R.
FEATURES
      Location/Qualifiers
          1..814
             /organism="Solanum tuberosum"
             /cultivar="kennebec"
             /db_xref="taxon:4113"
             /clone="cSTD7P13"
             /clone_lib="cSTD"
             /tissue_type="dormant tuber"
             /dev_stage="one month post-harvest"
             /lab_host="SOLR"
             /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
             XhoI; This library targets genes expressed in dormant
             tubers. This library was made from sections of dormant
             tuber, avoiding the buds and epidermis. Tubers were stored
             for one month post-harvest at 40C. The tuber was peeled,
             well away from the surface. Then it was chopped into 1-2
             mm cubes and immediately frozen in liquid nitrogen. This
             library is noted as P4 in tanksley lab notebooks."
BASE COUNT      242 a      146 c      191 g      235 t
ORIGIN
Query Match      26.7%; Score 456.8; DB 12; Length 814;
Best Local Similarity 73.3%; Pred No. 1.8e-75;
Matches 597; Conservative 0; Mismatches 217; Indels 0; Gaps 0;
QY 438 GCGTGAAGCTGCAAGCTTATTAAAGACGATCTTGGTGTGTTGAGGCTTGTCATTCTCT 497
Db 1 GAGAAAAGCTGCACAAATTGATGAAAACCTATTGTCAAAGTTGTGGAGGCTTGTCTCTCT 60
QY 498 TGGTGTATTGTCATAGAGATCTCAAACTGAGAAATTTCTGTTGATAGTCCCTAAAGATGA 557
Db 61 TGGGGTTATTGCAATAGAGATCTCAAACTGAGAAATTTCTTTTGTAGTCTCTGATGAAGA 120
QY 558 TGCTAAGCTTAAGGCTPACCGATTTTGGTTGTTCTGCTCTCTATTAAGCCAGGACAATATT 617
Db 121 TGCTAAGCTTAAGGCTACTGATTTGGTCTCTCTATTCTTATAAGCCAGGCGAGTATT 180
QY 618 ATATGACGTAGTTGGAGTCTGAGTGTGTTATCTCTACATTTTACTCAGCGGTGTTCC 677
Db 181 CTGAGATGTTTGGAAAGTCCATATTATGTTGCTCCTGAAGTTTGACAAATACTATGG 240
QY 678 ACCTGAATAGATGTTGGAGTCTGAGTGTGTTATCTCTACATTTTACTCAGCGGTGTTCC 737
Db 241 GCCTGAAATAGACGCTCTGGAGTCTGGAGTCACTCTTTATCTCTGTTATGTTGGGGTTC 300
QY 738 TCCCTCTCTGGGCGAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGAAAGTAGA 797
Db 301 TCCCTTTCTGGGCTGAGACAGACAATGGTATCTTCAACAGATATTAAAGGAAAGATAGA 360
QY 798 TTTCAAACTGACCGGTGGCCTACTATCTCAGAGCTCTAAAGATTGATCTATAAAAT 857
```

Db 361 CTTGAATCAGAACTTGGCCCTCAGATTTCTGATAGTCAAAAGATTTGGTAAGAAGAT 420  
QY 858 GGTGAAAGAGCCCAAGAAACGATTTCTGCTCATGAAGCCCTTGTGTCACCCATGGAT 917  
Db 421 GGTACACAGGATCCTAGAGCAGCATTAACCGCGCATCAAGTTCTATGTCTATCTTGGAT 480  
QY 918 TGTGATGAACAAGCAGCAGCAGCAGCAGCCTTGTGATCCAGCAGTCTTATCTGCTCTAAA 977  
Db 481 TGTGATGATATGTTGCTCCAGACAGCCCTTGGGTTCTGAGTTTGTGCGGCTTAA 540  
QY 978 GCAGTTTCTCAATGAATGAATTAAGAAATGCGATTACGGGTAATTCCTCAGAGACT 1037  
Db 541 GCAGTTCTATGATGAACAACCTTAAAGATGCTTACGAGCTATAGCAGAAAGGCT 600  
QY 1038 TFCAGAGGAGAAATGAGGCTGCAAGGATTTCAAGATGATGATGATGATGATGATGAT 1097  
Db 601 TFCAGAGGAGAAATGAGGCTGCAAGGATTTCAAGATGATGATGATGATGATGATGAT 660  
QY 1098 CGAAGCAGTACTTCTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCTGATCTGAACCTGAT 1157  
Db 661 TGAACATCATATGAGGACTTAAACATGTTTGAAGAGAGTAGGATCTGACTTAAC 720  
QY 1158 GGAATCAGAAATCAAGTCTCTCATGATGCGGCTGATATCAGACAGTGGTACATAGA 1217  
Db 721 AGAGTCCGAAATCAAGGCTTGTATGAGCGGCTGACTTTCAGACACAGGCACTATCGAC 780  
QY 1218 CTACGAGAAATTCCTAGCAGCAACCTTACACATG 1251  
Db 781 TATGGTGATTCATCGCTGCAACATTCGATTG 814

RESULT 9  
B28263/c  
LOCUS  
DEFINITION  
T8A20TFB TAMU Arabidopsis thaliana genomic clone T8A20, DNA  
sequence.  
B28263  
B28263.1 GI:2514229  
VERSION  
KEYWORDS  
SOURCE  
thale cress.  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 (bases 1 to 493)  
Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and  
Venter, J.C.  
Use of a BAC End Sequence Database To Identify Minimal Overlaps for  
Arabidopsis Genomic Sequencing  
Unpublished (1997)  
Other GSSs: T8A20TR  
Contact: Steve Rounsley  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: rounsley@tigr.org  
Seq primer: M13-21  
Class: BAC ends  
High quality sequence stop: 493.  
Location/Qualifiers  
1. .493  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone\_lib="T8A20"  
/sex="hermaphrodite"  
/notes="Vector: BelOBACII; Site\_1: HindIII; Site\_2: HindIII  
; Produced by Rod Wing"

FEATURES  
source  
126 a 110 C 95 G 162 t

ORIGIN  
Query Match 25.1%; Score 439; DB 17; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2.4e-70; Mismatches 0; Indels 0; Gaps 0;  
Matches 439; Conservative 0;  
QY 18 TTCTTTCTTCAAAATCGAGATCGAAGAGAACCAACCAAAAAACCAAAAAATGGAGACGAA 77  
Db 440 TTCTTTCTTCAAAATCGAGATCGAAGAGAACCAACCAAAAAACCAAAAAATGGAGACGAA 381  
QY 78 GCCAAACCTAGAGCGCTTCAACACAGTTCTACCATATCAACACACGATTAAAGAGA 137  
Db 380 GCCAAACCTAGAGCGCTTCAACACAGTTCTACCATATCAACACACGATTAAAGAGA 321  
QY 138 TCATTAGCTTCTGGAAAAAGCTAGGCCAAGCCCAATTTGGAACCAACCTATCTCTGAC 197  
Db 320 TCATTAGCTTCTGGAAAAAGCTAGGCCAAGCCCAATTTGGAACCAACCTATCTCTGAC 261  
QY 198 AGAGAAATCAACCTCCCTAATTTACGCTTCAATCGATTCGATTCATCATCTCTGAGCA 317  
Db 250 AGAGAAATCAACCTCCCTAATTTACGCTTCAATCGATTCGATTCATCATCTCTGAGCA 201  
QY 258 TCGGAGGATTAACCAAGATGTATGGCTGCAATTCAGATTCATCATCTCTGAGCA 141  
Db 200 TCGGAGGATTAACCAAGATGTATGGCTGCAATTCAGATTCATCATCTCTGAGCA 141  
QY 318 TCCAAATGTTCTAGGATCAAGGAGCTTATGAAGATTCGGTGTTCATATTTGTTAT 377  
Db 140 TCCAAATGTTCTAGGATCAAGGAGCTTATGAAGATTCGGTGTTCATATTTGTTAT 81  
QY 378 GGAGTTTGTGAAGTGGTGAAGCTTTTGTATCGATTTTGTCTTAAAGGTCATTTAGTGA 437  
Db 80 GGAGTTTGTGAAGTGGTGAAGCTTTTGTATCGATTTTGTCTTAAAGGTCATTTAGTGA 21  
QY 438 GCGTGAAGCTGTCAAGCTT 456  
Db 20 GCGTGAAGCTGTCAAGCTT 2

RESULT 10  
B11596/c  
LOCUS  
DEFINITION  
T8A20-T7 TAMU Arabidopsis thaliana genomic clone T8A20, DNA  
sequence.  
B11596  
B11596.1 GI:2092717  
VERSION  
KEYWORDS  
SOURCE  
thale cress.  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 (bases 1 to 1087)  
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and  
Ecker, J.  
BAC End Sequences at ATGC  
Unpublished (1997)  
Contact: Ecker J.  
Arabidopsis Thaliana Genome Center  
University of Pennsylvania  
Dept. of Biology, University of Pennsylvania, Philadelphia, PA  
19104  
Tel: 215-898-9384  
Fax: 215-898-8780  
Email: jecker@genome.bio.upenn.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 93  
High quality sequence stop: 873.  
Location/Qualifiers  
1. .1087  
/organism="Arabidopsis thaliana"  
/strain="Columbia"

FEATURES  
source

/db\_xref="taxon:3702"

/clone="T8A20"

/clone\_lib="TAMU"

/sex="hermaphrodite"

/note="Vector: BoloBACII; Site\_1: HindIII; Site\_2: HindIII

; Produced by Rod Wing"

BASE COUNT 308 a 206 c 178 g 392 t 3 others

ORIGIN

Query Match 25.1%; Score 437.8; DB 17; Length 1087;  
 Best Local Similarity 98.4%; Pred. No. 3.1e-70;  
 Matches 442; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 8 GTACATATCTCTCTCTCTCAATCGAGATCGAAGAGAACCAACCAAAACCAAAA 67

Db 495 GTTATCATCTCTCTCTCTCAATCGAGATCGAAGAGAACCAACCAAAACCAAAA 436

QY 68 TGGAGACGAAGCAAAACCCCTAGACGTCCTTCAAAACACACAGTTTACCATATCAAAACACAC 127

Db 435 TGGAGACGAAGCAAAACCCCTAGACGTCCTTCAAAACACACAGTTTACCATATCAAAACACAC 376

QY 128 GATTAGAGATCATTTACCTCTGGGAAAAAGCTAGGCGAAGCCCAATTTGGAACAACCT 187

Db 375 GATTAGAGATCATTTACCTCTGGGAAAAAGCTAGGCGAAGCCCAATTTGGAACAACCT 316

QY 188 ATCTCTGCACAGAGAAATCAACCTCCGCTAAATACGCTCGAAATCGATCCGGAAGGAA 247

Db 315 ATCTCTGCACAGAGAAATCAACCTCCGCTAAATACGCTCGAAATCGATCCGGAAGGAA 256

QY 248 AGCTCGTGTGCGGAGGATACGAAGATGATGCGGTGAATTCAGATCATCATCATC 307

Db 255 AGCTCGTGTGCGGAGGATACGAAGATGATGCGGTGAATTCAGATCATCATCATC 196

QY 308 TCTCTGAGCATCCAAATGTTGTAGGATCAAGGACACTATGCAAGATTCGGTGTTC 367

Db 195 TCTCTGAGCATCCAAATGTTGTAGGATCAAGGACACTATGCAAGATTCGGTGTTC 136

QY 368 ATATTGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTATCGGATTTTCTAAAGGTC 427

Db 135 ATATTGTTATGAGGTTTGTGAAGTGTGAGCTTTTGTATCGGATTTTCTAAAGGTC 76

QY 428 ATTTTAGTGAGCGTGAAGCTGCAAGCTT 456

Db 75 ATTTTAGTGAGCGTGAAGCTGCAAGCAT 47

RESULT 11

AI994248

LOCUS

701501524 A. thaliana, Ohio State clone set Arabidopsis thaliana

CDNA clone 701501524, mRNA sequence.

ACCESSION

AI994248

VERSION

AI994248.1

GI:5841153

KEYWORDS

EST.

SOURCE

Arabidopsis thaliana

thale cress.

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 528)

Chen, J., Momiya, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,

Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,

GorGene, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,

Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,

Policky, J., Suzuki, G., Argente, C., Shah, S., Nobrega, A., Murry, L.,

Turner, C., Krikorian, S., Elder, L., and Hansen, D.

Arabidopsis thaliana Gene Expression MicroArray

Unpublished (1999)

CONTACT: David Scoller, Ph.D.

Genome Systems, Inc., a wholly owned subsidiary of Incyte

Pharmaceuticals, Inc.

4633 World Parkway Circle, St. Louis, MO 63134, USA

Fax: 314-427-3324

Email: service@genomesystems.com.

Location/Qualifiers

Source

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/clone="701501524"

/clone\_lib="A. thaliana, Ohio State clone set"

/note="cDNA library was made from selected clones from the

Arabidopsis thaliana Ohio State clone set."

BASE COUNT 160 a 100 c 136 g 132 t

ORIGIN

Query Match 24.3%; Score 424.8; DB 9; Length 528;

Best Local Similarity 92.3%; Pred. No. 9.1e-68;

Matches 480; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 925 GAACAAGCAGCAGACCAAGCCTCTTGATCCACGACGCTTATCTCTCTTAAGCAGTTT 984

Db 6 GAACAAGCAGCAGCAGACCAAGCCTCTTGATCCACGACGCTTATCTCTCTTAAGCAGTTT 65

QY 985 TCTCAATGAATTAAGATTAAAGAAATGCGATTACGGGTAATTTGCTGAGAGACTTTCAGAG 1044

Db 66 TCTCAATGAATTAAGATTAAAGAAATGCGATTACGGGTAATTTGCTGAGAGACTTTCAGAG 125

QY 1045 GAAGAAATGGAGGCTCTGAAGGATTTCTCAAGATGTAGACACAGACACAGCGGNAACG 1104

Db 126 GAAGAAATGGAGGCTCTGAAGGATTTCTCAAGATGTAGACACAGACACAGCGGNAACG 185

QY 1105 ATTACTTTTGAA-GAGCTCAAAAGCGGTTTGAAGAGAGTCGGATCTGAACTGATGAATC 1163

Db 186 ATTACTTTTGAAAGAGGCTCAAAAGCGGTTTGAAGAGAGTCGGGCTTTAACTGGTGAATC 245

QY 1164 AGAATCAAGTCTCTCATGATGGGCTGATATCGACAAAGTGGTACATAGACGTTACGG 1223

Db 246 AGAATCAAGTCTCTCATGATGGGCTGATATCGGCAACAGTGGTACATAGACGTTACGG 305

QY 1224 AGAATTCCTAGCAGCAACCTTACACATGAACAGATGAGAGAGAGAGATTTCTGGTGGC 1283

Db 306 AGAATTCCTAGCAGCAACCTTACCATGACACAGATGAGAGAGAGAGATTTCTGGTGGC 365

QY 1284 TGCATTTTCGGAC-TTTGCAAAAGCAGGAGCGGTTATATCACATCGATGAGCTTCAGT 1342

Db 366 TGCCTTTTCGTACTTTTGCAAAAGCAGGAGCGGTTATATCACAAATCGATGA-CTTCAT 424

QY 1343 CAGCTTGCACAGAGTTTGGTCTATGTATACCTCTGGACGACATGATCAAGGAGATTG 1402

Db 425 CAATTTGCACAGGTTTGGTCTATGTATTAACCTTGGAGCATTTGCCAGGGGATTG 484

QY 1403 ATCTTGACAAATGACGGAAGATCGATTTCGGAGTTTAC 1442

Db 485 GTCTTTACAATGACGGGAAATCGGTTTCTCGGGGTTTC 524

RESULT 12

BG596613

LOCUS

EST495291 cSTS Solanum tuberosum

DEFINITION

mRNA sequence.

ACCESSION

BG596613

VERSION

BG596613.1

GI:13614753

KEYWORDS

EST.

SOURCE

Solanum tuberosum

potato.

ORGANISM

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; eurosids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 742)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chieningo, A.,

Bougrin, C., Suel, C.K., Ronning, C., Tanksley, S. and Baker, B.

Generations of ESTs from sprouting potato eyes

Unpublished (2000)

CONTACT: Cathy Ronning



346 ATGAGATTCCGGTGTGTTTCATATTTATGAGGTTTGTGAGGTGTTGAGGTTGTTGAGCTTTT 405  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 331 TACGAGGATTGGTTTCTGTTCAATTTGTTATGAGCTTTGTGAGGTGTTGAGGTTGTTGTT 390  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 406 GATCGATTGTTTCTTAAGGTCATTTAGTGAAGCTGTAAGCTGTCACGCTTATTAAGAG 465  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 391 GATAGATTGTGAGAAAGGCAATTAATAGTGAAGACAAGCTGCTAAGTTGATTAGAACT 450  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 466 ATTCTGTGTTGTTGAGGCTTGTCATTTCTCTTGGTGTATGATAGATCTCAAACT 525  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 451 ATTGTGAGGTTGTTGAAGCTTGTCATTTCTTGGAGTTATGACAGAGACCTTAAACCT 510  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 526 GAGATTTCTTTGTTGATAGTCCCTAAAGATGATGCTAAGCTTAAGGTACGATTTGGT 585  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 511 GAGATTTTGTGTTGATCTGTTGATGAAGATGCTCTTCTCAAAATATATGATTTTGGT 570  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 586 TTGCTGTCTCTTATTAAGCCAGGCAATATTTATGACGTAGTTGGAAGTCCGCTACT 645  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 571 TTGCTGTTTATACAGCCAGGTGAATCTTTAGTGATGTTGTTGGAAGCCATAT 630  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 646 GTTGACAGAGTCTTAAGAAATGTTATGAGCTGAATAGATGTGTGAGTG-CTGG 704  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 631 GTTGCCAGAGTCTTGCACAAATATATGAGCTGAAGCAGACGTGTGAGTGCCTGG 690  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 705 TGTATCTCTACTATTTACTCAGCGGTGTTCCCTCTTCTGCGCAGAGACTGAGTCTGG 764  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 691 TGTATTTGATACCTTATTAAGCGGGTGTCTCCGTTTGGCCAGACCGCATCAAGG 750  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 765 AATCTTAGACAGATTGCAAGGGAATGATTTCAATCTGACCGGTGGCTACTAT 824  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 751 GATCTTCACACAGAT-TTTCAGGAAACCTTGATTTCCGGTCTGAGCGGTGGCTGGAT 809  
 2y | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 825 CTCA 828  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 810 TTCA 813

RESULT 14  
 Bi178776  
 LOCUS EST519721 cSTE Solanum tuberosum cDNA clone cSTE15P12 5' sequence,  
 DEFINITION mRNA sequence.  
 ACCESSION Bi178776  
 VERSION Bi178776.1 GI:14644587  
 KEYWORDS EST.  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 686)  
 van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Cho,J.,  
 Chlemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and  
 Baker,B.  
 TITLE Generation of ESTs from in vitro grown microtubers  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Cathy Ronning  
 The Institute for Genomic Research  
 For clone info: please contact Research Genetics, Libraries  
 Division tel 1-800-711-6195, email cdna@resgen.com  
 Seq primer: M13P-R.  
 FEATURES  
 source  
 1..686  
 /organism="Solanum tuberosum"  
 /cultivar="Bintje"  
 /db\_xref="taxon:4113"  
 /clone="cSTE15P12"  
 /clone\_lib="cSTE"  
 /tissue\_type="axillary buds of stem explants; growing  
 sink-tubers"  
 /dev\_stages="7, 8 and 10 days"  
 /lab\_host="SOLR"

RESULT 15

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Tissue supplied by Christian Bachem and Richard  
 Visser (Department of Plant Breeding, Wageningen  
 University, The Netherlands). The cSTA libraries will  
 attempt to capture the induction and initiation/initial  
 growth of the tuber in an in vitro system as described in  
 Bachem et al. (Plant Journal, 1996). Small microtubers  
 develop from axillary buds attached to stem explants when  
 placed on a high sucrose medium (10%). Visible  
 morphological changes occur synchronously at day five in  
 the axillary buds. The first library, cSTA (1-20) consists  
 of axillary buds harvested on days 1-3. This targets  
 those genes involved in induction of the microtubers. The  
 following libraries, cSTA (21-40) and cSTA (41-60)  
 capture genes involved in tuber initiation and outgrowth.  
 This library is noted as P3 in Tanksley lab notebooks."

BASE COUNT 198 a 122 c 162 g 204 t

ORIGIN

Query Match 23.0%; Score 401.8; DB 13; Length 686;

Best Local Similarity 74.2%; Pred. No. 1.3e-63;

Matches 508; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 442 GAAGCTGTCAAGCTTATTAAGACGATTCCTTGGTGTGTTGAGGCTTGTCTATCTCTTGGT 501

Db 1 GAAGCTGTCTAAATGATCAAAACAATTTGTTGGGTGGTGAAGCTTGCCATTCATTAGGG 60

Qy 502 GTTATGATAGAGATCTCAACCTGAGAAATCTTGTGATAGTCTTAAGATGATGCT 561

Db 61 GTTATGACAGAGATCTCAAGCCCTGAGAAATCTTGTGTTCTTAGTCTCAAGAGATGCT 120

Qy 562 AAGCTTAAGGCTACCGATTTTGGTTCCTCTCTTCTATAAGCCAGGACAATATTTATAT 621

Db 121 GCTCTCAAGGCCACTGATTTTGGCTTCTGTTTCTATAAGCCAGGTGAACATTTCT 180

Qy 622 GACGTAGTTGGAAGTCGCTACTATGTTGCACAGAGGTGCTTAAGAAATCTTATGACCT 681

Db 181 GATGTGTGGAAGTCTCTTATATGTTGCCCCAGAGGTTTATGCAAGCATTTATGACCT 240

Qy 682 GAAATAGATGTGTGAGTGTGTTGTTATCTCTACATTTTACTCAGCGGTGTTCTCC 741

Db 241 GAATCAGATGTATGAGTGCAGGAGTTATCTTGTACATATTTACTTAGTGTGTTCCACCT 300

Qy 742 TTCTGGGACAGATCTGAGTCTGGAACTTTTAGACAGATATTCGAAGGAAAGTTAGATTTC 801

Db 301 TTTTGGGACAGAACTGATATGGGAATATTTGTCAGATCTGCGAGGCAAACTAGATTTA 360

Qy 802 AAATCTGACCGTGGCTTACTATCTCAGAAGCTGCTAAAGATTTGATCTATAAAATGCTC 861

Db 361 GAATCCGAACTTGGCTTGGNAATTTAGATAGTGAAGGATTTGATACCAAAATCTT 420

Qy 862 GAAAGGACCCCAAGAAACGCAATTTCTGCTCATGAAGCTTGTGTCACCATGAGATTGTC 921

Db 421 GATAGAAATCCAAAGAGAGGTTAACTGCCCATGAAGTTTGTGCCATCGTGGATCGTG 480

Qy 922 GATGAACAAGCAGACAGACCAAGCCCTCTTGATCCAGAGCTCTTCTCTGCTTAAAGCAG 981

Db 481 GATGACTCAATGACCCCTGATPAACCTTCTTGATTTCTCAGTTCTTTTACGCCCTCAAGCAA 540

Qy 982 TTTTCTCAAAATGAATTAAGAAATGCAAAATGCGATTACGGTAAATTTGCTGAGAGACTTCA 1041

Db 541 TTCTCAGCAATGAACAAACTAAAGAAATGCGTTTGGGTGTGATTTGCCGAGAGGCTATCA 600

Qy 1042 GAGGAGAAATGGAGGTCTGAAGGAATTTGTCAGATGATAGACAGACAGACAGCGGA 1101

Db 601 GAAGAGGAGATTGTTGGCCCTCAAGGAGCTATTCAAAATGTTAGACAGACAAATAGTGGGA 660

Qy 1102 ACGATTACTTTTGAAGAGCTCAAG 1126

Db 661 AACATAACCTTTTGGAACATAAAG 685

B0865474  
LOCUS B0865474  
DEFINITION QGCSA16.Vg.abl QG ABCDI lettuce salinas Lactuca sativa linear EST 14-AUG-2002  
ACCESSION B0865474  
VERSION B0865474.1 GI:22250939  
KEYWORDS EST.  
SOURCE Lactuca sativa.  
ORGANISM Lactuca sativa.  
REFERENCE Lactuca sativa.  
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L., and Bradford, K.  
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project  
JOURNAL http://comgenomics.ucdavis.edu/  
COMMENT Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
belongs to contig QG\_CA\_Contig3691, see http://cgdb.ucdavis.edu/  
for details.  
Plate: QGCS row: A column: 16.  
FEATURES  
source  
1. .751  
Location/Qualifiers  
/organism="Lactuca sativa"  
/cultivar="Salinas"  
/db\_xref="taxon:4236"  
/clone="QGCSA16"  
/clone\_lib="QG ABCDI lettuce salinas"  
/lab\_host="E.coli"  
/note="Vector: pBRCDNAS1AB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/  
TAG LIB=QG ABCDI lettuce salinas  
TAG TISSUE=chemical induction  
TAG\_SEQ=GTAGCCGGG"  
BASE COUNT 218 a 117 c 180 g 236 t  
ORIGIN  
Query Match 22.3%; Score 388.8; DB 14; Length 751;  
Best Local Similarity 70.9%; Pred. No. 3e-61;  
Matches 530; Conservative 0; Mismatches 217; Indels 1; Gaps 1;  
QY 287 AGATTGAGATCATGCTATCTCTCTGAGCATCCAAATGTTCTTAGGATCAAGGACTT 346  
Db 1 AGATTGAGATCATGCTATCTCTGAGCATCCAAATGTTCTTAGGATCAAGGACTT 60  
QY 347 ATGAAGATTCGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 406  
Db 61 ATGAAGATTCGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120  
QY 407 ATCGATTGTTTCTAAAGTCAATTTTAGTGAGCGTGAAGCTGTCAGCTTATTAAAGCA 466  
Db 121 ATAGGATTATTCAAGAGGACATTACACTGAAAAAAGAGCAGCTGAGCTTACAGAGCA 180  
QY 467 TTCTGTGTGTTGTTGAGGCTTGCTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 526  
Db 181 TTGTGGGTTGTGGAGACTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 240

QY 527 AGAATTTCTTTGTTGATAGTCTTAAGATGATGCTTAAGCTTAAGGCTACCGATTTGGTT 586  
Db 241 AAAATTTCTTTGTTGATAGTCTTAAGATGATGCTTAAGCTTAAGGCTACCGATTTGGTT 300  
QY 587 TGTCTGTCTCTATATAAGCCAGGACAATATTATATATGACGTAGTTGGAAGTCCGTACTATG 646  
Db 301 TATCGGTTTCTTCAAAACAGGTGATCAITTAATGATGTGGTTGAAGCCCATATTATG 360  
QY 647 TTGCACACAGAGTCTTAAAGAAATGTTATGAGCCTGAAATAGATGTGGAGTGTGGTG 706  
Db 361 TTGCACACAGAGTCTTAAAGAAATGTTATGAGCCTGAAATAGATGTGGAGTGTGGTG 420  
QY 707 TTAATCTCTACATTTTACTCAGCGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 766  
Db 421 TTAATGTTTATATCTCTTATTAAGTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
QY 767 TCTTTAGACAGATTTGCAAGGGAAGTTAGATTTCAAAATCTGACCCGTGGCCCTTACTTCT 826  
Db 481 TATTTGAACAAGTCTCTCAAGGCGATCTTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540  
QY 827 CAGAAGCTGCTAAAGATTTGATCTATAAATGCTCGAAGAGCCCCCAAGAACGCAATTT 886  
Db 541 CTGAAGATGCAAAAAGATCTTGAAGGAGATGCTTATTCGAGACCCCTTAAAGACGATTA 600  
QY 887 CTGCTCATGAAGCCCTTGTGTCAACCCATGGATTTGCGATGAACAAGCAGCACCAGACAAGC 946  
Db 601 CTGCACATGAAGTTTATGTCATCTTTGGGTTCAAGTTGATGGCGTGGCTCCAGACAAGC 660  
QY 947 CTCCTGATCCAGAGTCTTATCTCTGTTAAAGCAGTTTCTCAAAATGAATTAAGATAAGA 1006  
Db 661 CTCCTGACTCTGCACTCTTAAGTGAATGAA-CAATTTTCAGCCATGAATTAAGCTTTAGA 719  
QY 1007 AAATGGCATTACGGGTAAATGCTCGAGAG 1034  
Db 720 AAATGGCTTTGAGGTTATAGCTGAGAG 747

Search completed: February 13, 2003, 19:51:19  
Job time : 2599 secs